

| ID | HV3G_HUMAN | STANDARD: | PRT: | 122 AA. |
|---|--|-----------|------|---------|
| AC | P01768; | | | |
| DT | 21-JUL-1986 (Rel. 01, Created) | | | |
| DT | 21-JUL-1986 (Rel. 01, Last sequence update) | | | |
| DT | 15-SEP-2003 (Rel. 42, Last annotation update) | | | |
| DE | Ig heavy chain V-II region C.M. | | | |
| OS | Homo sapiens (Human). | | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | |
| OC | Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo. | | | |
| OX | NCBI_TaxID=9606; | | | |
| RN | [1] | | | |
| RP | SEQUENCE. | | | |
| RX | MEDLINE=81013859; PubMed=6774332; | | | |
| RA | Lehman D.W., Putnam F.W.; | | | |
| RT | "Amino acid sequence of the variable region of a human mu chain: | | | |
| RT | location of a possible JH segment."; | | | |
| RL | Proc. Natl. Acad. Sci. U.S.A. 77:3239-3243(1980). | | | |
| CC | -1- MISCELLANEOUS: THIS MU CHAIN WAS ISOLATED FROM THE PLASMA OF A | | | |
| CC | PATIENT WITH MACROGLOBULINEMIA. | | | |
| CC | -1- SIMILARITY: Contains 1 immunoglobulin-like domain. | | | |
| DR | HSP; P01772; 2F84. | | | |
| DR | HSSB; P01772; 2F84. | | | |
| DR | GO; GO:0005576; C:cytoregulatory; NAS. | | | |
| DR | GO; GO:0003823; P:antigen binding activity; NAS. | | | |
| DR | GO; GO:0006955; P:immune response; NAS. | | | |
| DR | InterPro; IPR007110; IG-1-like. | | | |
| DR | InterPro; IPR003006; IG_MHC. | | | |
| DR | InterPro; IPR003596; IG_V. | | | |
| DR | Pfam; PF00047; Ig_1. | | | |
| DR | SMART; SM00406; IGV; 1. | | | |
| DR | PROSITE; PS50835; IG_LIKE; 1. | | | |
| KW | Immunoglobulin V region; Pyrolydine carboxylic acid. | | | |
| FT | DOMAIN 1 112 | | | |
| FT | MOD_RES 1 1 | | | |
| FT | NON_TER 122 122 | | | |
| SQ | SEQUENCE 122 AA; 13668 MW; A42D0F17D252F1C2 CRC64; | | | |
| Query Match | | | | |
| Best Local Similarity 68.8%; Score 460.5; DB 1; Length 122; | | | | |
| Matches 85; Conservative 19; Mismatches 17; Indels 5; Gaps 2; | | | | |
| QY | 1 QVKLLBSGGGVQVPGGSLRVACVAGSGFTFRNGGHWVROAPGKGLGFWAFIFPDASNKGY 60 | | | |
| DB | 1 QVELVBSGGGVVZPGSLRLSCAASGFTFSNMYMVRPFGKGLGFWAIVSYBGBKTY 60 | | | |
| QY | 61 GDSVGRFLVSRDNSKNTLYLQMGGLRAEDTAVVYCARBKAVRGISR--YNYMDVWGKGT 119 | | | |
| DB | 61 AASVGRFLVSRDNSKNTLYLQMGSLRAEDTAVVYCARBKAVRGISR--YNYMDVWGKGT 116 | | | |
| QY | 120 TVTVSS 125 | | | |
| DB | 117 LTVVSS 122 | | | |
| RESULT 3 | | | | |
| ID | HV16_MOUSE | STANDARD; | PRT; | 136 AA. |
| AC | P01783; | | | |
| DT | 21-JUL-1986 (Rel. 01, Created) | | | |
| DT | 21-JUL-1986 (Rel. 01, Last sequence update) | | | |
| DT | 15-SEP-2003 (Rel. 42, Last annotation update) | | | |
| DE | Ig heavy chain V region MOPC 21 precursor (Fragment). | | | |
| OS | Mus musculus (Mouse). | | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | |
| OC | Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. | | | |
| OX | NCBI_TaxID=10090; | | | |
| RN | [1] | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RX | MEDLINE=81234548; PubMed=6788376; | | | |
| RA | Bothwell A.U.M., Faabind M., Rech M., Imanishi-Kari T., Rajewsky K., | | | |
| RA | Baltimore D.; | | | |

| Query Match | Best Local Similarity | Score | DB 1 | Length | DB 2 |
|--|---|--------|---------|--------|-------|
| Matches 83; Conservative 16; Mismatches 19; Indels 7; Gaps 2 | 66.4%; Pred. No. 1.1e-37; | 433.5; | DB 1; | 136; | DB 2; |
| QY | 2 VKLSEGGGVQPGGSLRVCVAGSFTFRNFMWVRQAPGKGLRWVAFIMFDASNKGYG 61 | | | | |
| DB | 18 VQLVESGGGLVQPGGSRKLSCAASGFTFSRGMWVRQAPGKGLRWVAFIMFDASNKHYA 77 | | | | |
| QY | 62 DSVKGRFTVSDNSKNTLYLQMGRLARDTVVYGCAREKAVRGISRYNYV -MDVNGSGT 120 | | | | |
| DB | 78 DTVKGRFTISRNPNTLFLQVTSLSRSEDITMYTCAR-----WGNYYRYAMDYGGGTS 131 | | | | |
| QY | 121 TVVSS 125 | | | | |
| DB | 132 TVVSS 136 | | | | |
| RESULT 4 | | | | | |
| HVJK HUMAN | | | | | |
| ID HVJK HUMAN | STANDARD; | PRT; | 126 AA. | | |
| AC P01772; | | | | | |
| DT 21-JUL-1986 (Rel. 01, Created) | | | | | |
| DT 21-JUL-1986 (Rel. 01, Last sequence update) | | | | | |
| DT 15-SEP-2003 (Rel. 42, Last annotation update) | | | | | |
| DE Ig heavy chain V-II region KOL. | | | | | |
| OS Homo sapiens (Human) | | | | | |
| OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | | | |
| OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo. | | | | | |
| OX NCBI_TaxID=9606; | | | | | |
| RN [1] | | | | | |
| RP SEQUENCE, AND DISULFIDE BONDS. | | | | | |
| RX MEDLINE=83289131; PubMed=6884994; | | | | | |

RA Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;
 RT "Three-dimensional structure determination of antibodies. Primary
 structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.";
 RL Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).

RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).

RE MEDLINE=81072295; PubMed=7441755;

RA Marguier M., Deisenhofer J., Huber R., Palm W.;

RT "Crystallographic refinement and atomic models of the intact
 immunoglobulin molecule KOL and its antigen-binding fragment at 3.0 A
 and 1.0 A resolution.";

RT J. Mol. Biol. 141:369-391(1980).

RL J. Mol. Biol. 141:369-391(1980).

CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.

DR PIR; A02055; G1HUKL.

DR PDB; 2F84; 12-JUL-89.

DR PDB; 2IC3; 12-JUL-89.

DR GO; GO:0005576; C:extracellular; NAS.

DR GO; GO:0003823; F:antigen binding activity; NAS.

DR GO; GO:0006955; P:immune response; NAS.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003006; Ig_MHC.

DR InterPro; IPR003596; Ig_V.

DR Pfam; PF00047; Ig; 1.

DR SMART; SM00406; IgV; 1.

DR PROSITE; PS50835; IG_LIKE; 1.

KW Immunoglobulin V region; 3D-structure; Pyrrolidone carboxylic acid.

FT DOMAIN 1 112 IG-LIKE.

FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.

FT DISULFID 22 96

FT DISULFID 105 110

FT STRAND 3 7

FT STRAND 11 12

FT STRAND 14 15

FT STRAND 18 25

FT HELIX 29 31

FT STRAND 34 39

FT TURN 41 42

FT STRAND 45 51

FT TURN 53 54

FT STRAND 58 60

FT HELIX 62 64

FT STRAND 65 65

FT TURN 66 67

FT STRAND 68 73

FT TURN 74 77

FT STRAND 78 83

FT HELIX 88 90

FT STRAND 92 99

FT STRAND 106 106

FT TURN 107 108

FT STRAND 109 109

FT STRAND 113 116

FT STRAND 120 124

FT NON_TER 126 126

SO SEQUENCE 126 AA; 13718 MW; E4D71B52B16F8776 CRC64;

Query Match 64.1%; Score 428.5; DB 1; Length 126;

Best Local Similarity 65.1%; Pred. No. 3,4e-37; Indels 1; Gaps 1;

Matches 82; Conservative 19; Mismatches 25; Indels 1; Gaps 1;

QY 1 QVLTLESGGVVOPGSLRVACVAGFTFRNFGMHVWROAPGKLEWVAFIWDASNGY 60

DB 1 QVLTLESGGVVOPGSLRVACVAGFTFRNFGMHVWROAPGKLEWVAFIWDASNGY 60

QY 61 GDSVKGKFTVSRDNTSLTYLQNNGLRAEDTAVYYCAREKAVGISRNYNY-MDVWGKGT 119

DB 61 ADSVKGKFTVSRDNTSLTYLQNNGLRAEDTAVYYCAREKAVGISRNYNY-MDVWGKGT 119

QY 120 TVTVSS 125

DB 121 PTVVSS 126

QY 121 PTVVSS 126

DB 121 PTVVSS 126

RESULT 5

ID HV31_HUMAN

AC P01770

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE Ig heavy chain V-II region NIE.

OS Homo sapiens (human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE.

RX MEDLINE=77070269; PubMed=826475;

RA Ponstingl H., Hilschmann N.;

RT "The rule of antibody structure. The primary structure of a
 monoclonal IgG1 immunoglobulin (myeloma protein NIE). III. The
 chymotryptic peptides of the H-chain, alignment of the tryptic
 peptides and discussion of the complete structure.";

RT Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).

RL [2]

CC DISULFIDE BOND.

CC MEDLINE=77070267; PubMed=1002129;

RA Dreker L., Schwarz J., Reichel W., Hilschmann N.;

RT "Rule of antibody structure. The primary structure of a monoclonal
 IgG1 immunoglobulin (myeloma protein NIE). I: Purification and
 characterization of the protein, the L- and H-chains, the
 cyanogen bromide cleavage products, and the disulfide bridges.";

RT Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).

RL [1]

CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGK1 MYELOMA
 PROTEIN.

CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.

DR PIR; A91668; G1HUKL.

DR HSSP; P01772; 2F84.

DR GO; GO:0005576; C:extracellular; NAS.

DR GO; GO:0003823; F:antigen binding activity; NAS.

DR GO; GO:0006955; P:immune response; NAS.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003006; Ig_MHC.

DR InterPro; IPR003596; Ig_V.

DR Pfam; PF00047; Ig; 1.

DR SMART; SM00406; IgV; 1.

DR PROSITE; PS50835; IG_LIKE; 1.

KW Immunoglobulin V region; 3D-structure; Pyrrolidone carboxylic acid.

FT DOMAIN 1 112 IG-LIKE.

FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.

FT DISULFID 22 96

FT NON_TER 119 119

SO SEQUENCE 119 AA; 13242 MW; C96935A6B55E165B CRC64;

Query Match 62.3%; Score 417; DB 1; Length 119;

Best Local Similarity 63.2%; Pred. No. 4,8e-36;

Matches 79; Conservative 19; Mismatches 21; Indels 6; Gaps 2;

QY 1 QVLTLESGGVVOPGSLRVACVAGFTFRNFGMHVWROAPGKLEWVAFIWDASNGY 60

DB 1 QVLTLESGGVVOPGSLRVACVAGFTFRNFGMHVWROAPGKLEWVAFIWDASNGY 60

QY 61 GDSVKGKFTVSRDNTSLTYLQNNGLRAEDTAVYYCAREKAVGISRNYNY-MDVWGKGT 120

DB 61 ADSVKGKFTVSRDNTSLTYLQNNGLRAEDTAVYYCAREKAVGISRNYNY-MDVWGKGT 120

QY 121 TVTVSS 125

DB 121 PTVVSS 119

QY 121 PTVVSS 119

DB 121 PTVVSS 119

QY 121 PTVVSS 119

DB 121 PTVVSS 119

QY 121 PTVVSS 119

DB 121 PTVVSS 119

QY 121 PTVVSS 119

DB 121 PTVVSS 119

QY 121 PTVVSS 119

DB 121 PTVVSS 119

QY 121 PTVVSS 119

DB 121 PTVVSS 119

QY 121 PTVVSS 119

DB 121 PTVVSS 119

QY 121 PTVVSS 119

DB 121 PTVVSS 119

QY 121 PTVVSS 119

DB 121 PTVVSS 119

QY 121 PTVVSS 119

DB 121 PTVVSS 119

QY 121 PTVVSS 119

DB 121 PTVVSS 119

DT 21-JUL-1986 (Rel. 01, last sequence update)
 DT 15-SEP-2003 (Rel. 42, last annotation update)
 DE Ig heavy chain V-II region GA.
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE
 RX MEDLINE=74175307; PubMed=4208843;
 RA Florent G., Lehman D., Putnam F.W.;
 RT "The switch point in mu heavy chains of human Igm immunoglobulins.";
 RL Biochemistry 13:2482-2498(1974).
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S
 CC MACROGLOBULIN.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
 DR PIR; A02052; M3HUGA.
 DR HSSP; P01772; 2PB4.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding activity; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003006; IG_MHC.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IgV; 1.
 DR PROSITE; PS50835; IG LIKE; 1.
 KW Immunoglobulin V region; Pyroliidone carboxylic acid.
 FT DOMAIN 1 112
 FT MOD_RES 1 112 PYROLIDONE CARBOXYLIC ACID.
 FT NON_TER 1 122
 SQ SEQUENCE 122 AA; 13166 MW; 74E5B6959E84100A CRC64;
 Query Match 60.9%; Score 407.5; DB 1; Length 122;
 Best Local Similarity 56.6%; Pred. No. 4.7e-35;
 Matches 73; Conservative 25; Mismatches 20; Indels 11; Gaps 2;
 QY 1 QVLTLESGGGVVGPGSLRVACVAGSGFTFRNFGMHVWRQAPGKLEWAFIMPDASNKGY 60
 DB 1 EVKLISGCGGLVPGGSLKSCAASGDFSRVWMSWRQAPGKLEWIGINPDSSRTNY 60
 QY 61 GDSVKGRFTVSRNSKNTLYLQWNGLRADPTAVYYCARE---KAVRGISRYNYMDVWG 116
 DB 61 AASVKGRFTISRBSKNTLYLQWNGLRADPTAVYYCARE---KAVRGISRYNYMDVWG 116
 QY 117 KGTIVTSS 125
 DB 114 ZGLTVTSS 122
 RESULT 7
 HV38 MOUSE STANDARD; PRT; 119 AA.
 AC P01808;
 DT 21-JUL-1986 (Rel. 01, last sequence update)
 DT 15-SEP-2003 (Rel. 42, last annotation update)
 DE Ig heavy chain V region T601.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sclatognathi; Muridae; Murinae; Mus.
 NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=79223895; PubMed=111245;
 RA Rao D.N., Rudikoff S., Krutzsch H., Potter M.;
 RT "Structural evidence for independent joining region gene in
 RT immunoglobulin heavy chains from anti-galactan myeloma proteins and
 RT its potential role in generating diversity in
 RT complementarity-determining regions.";
 RL Proc. Natl. Acad. Sci. U.S.A. 76:2890-2894(1979).
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGA MYELOMA PROTEIN
 CC THAT BINDS GALACTAN.

CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
 DR PIR; A02078; AVM5T6.
 DR HSSP; P01810; 2PB4.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IgV; 1.
 DR PROSITE; PS50835; IG LIKE; 1.
 KW Immunoglobulin V region.
 FT DOMAIN 1 112
 FT NON_TER 1 119
 SQ SEQUENCE 119 AA; 13169 MW; BC38CC84E6EA00E8 CRC64;
 Query Match 60.3%; Score 403.5; DB 1; Length 119;
 Best Local Similarity 62.4%; Pred. No. 1.2e-34;
 Matches 78; Conservative 18; Mismatches 22; Indels 7; Gaps 2;
 QY 1 QVLTLESGGGVVGPGSLRVACVAGSGFTFRNFGMHVWRQAPGKLEWAFIMPDASNKGY 60
 DB 1 EVKLISGCGGLVPGGSLKSCAASGDFSRVWMSWRQAPGKLEWIGINPDSSRTNY 60
 QY 61 GDSVKGRFTVSRNSKNTLYLQWNGLRADPTAVYYCAREKAVRGISRYNYMDVWGCTT 120
 DB 61 TPELKKRFTISRBNKNTLYLQWNGLRADPTAVYYCAREKAVRGISRYNYMDVWGCTT 113
 QY 121 VTVSS 125
 DB 114 VTVSS 118
 RESULT 8
 HV3D HUMAN STANDARD; PRT; 115 AA.
 AC P01765;
 DT 21-JUL-1986 (Rel. 01, last sequence update)
 DT 15-SEP-2003 (Rel. 42, last annotation update)
 DE Ig heavy chain V-II region TIL.
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=78005528; PubMed=409716;
 RA Wang A.-C., Wang I.Y., Fudenberg H.H.;
 RT "Immunoglobulin structure and genetics. Identity between variable
 RT regions of a mu and a gamma2 chain.";
 RL J. Biol. Chem. 252:7192-7199(1977).
 CC -1- MISCELLANEOUS: THE SEQUENCES OF THE V REGIONS OF THE HEAVY CHAINS
 CC OF IGM AND IGG2 ISOLATED FROM A SINGLE PATIENT WITH BICLONAL
 CC GAMMOPATHY ARE IDENTICAL. THEIR LIGHT CHAINS ARE APPARENTLY ALSO
 CC IDENTICAL.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
 DR PIR; A02048; H3HUTL.
 DR HSSP; P01772; 2PB4.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding activity; NAS.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IgV; 1.
 DR PROSITE; PS50835; IG LIKE; 1.
 KW Immunoglobulin V region.
 FT DOMAIN 1 108
 FT NON_TER 1 115
 SQ SEQUENCE 115 AA; 12356 MW; 4DCC67D179F62326 CRC64;
 Query Match 59.9%; Score 401; DB 1; Length 115;
 Best Local Similarity 62.4%; Pred. No. 2.1e-34;

| Matches | 78; Conservative | 16; Mismatches | 21; Indels | 10; Gaps | 2; |
|---|--|----------------|------------|----------|-----|
| Qy | 1 QVKLLIEGGGVQPGSGSLRVACVAGSFFTRNFGMHWVQAPGKGLIEWAFTIFDASNKGY | | | | 60 |
| Db | 1 EVQLLEISGGGLVQPGGSLRLSCAASGFFSTYVMWVQAPGKGLZMWGALIZGSLVSZSY | | | | 60 |
| Qy | 61 GDSVVGRTFVSNDNSKNTLYLQNNGLRADDTAVVYCAREKAVRGISRYNYWMDVWGKGT | | | | 120 |
| Db | 61 ABSVVGRTTISRNDNSKNTL---MNSLRADDTAVVYCAKGVSA-----YTFBYWGZGTL | | | | 110 |
| Qy | 121 TVVSS 125 | | | | |
| Db | 111 TVVSS 115 | | | | |
| RESULT 9 | | | | | |
| HV30_HUMAN | | | | | |
| ID | HV30_HUMAN | STANDARD; | PRT; | 117 AA. | |
| AC | P01776; | | | | |
| DT | 21-JUL-1986 (Rel. 01, Created) | | | | |
| DT | 21-JUL-1986 (Rel. 01, Last sequence update) | | | | |
| DT | 15-SEP-2003 (Rel. 42, Last annotation update) | | | | |
| DE | Ig heavy chain V-II region WAS. | | | | |
| OS | Homo sapiens (Human). | | | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | | |
| OC | Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. | | | | |
| OC | NCBI_TaxID=9606; | | | | |
| RN | [1] | | | | |
| RP | SEQUENCE. | | | | |
| RX | MEDLINE=74142702; PubMed=4522793; | | | | |
| RA | Capra J.D., Kehoe J.M., | | | | |
| RT | "Variable region sequences of five human immunoglobulin heavy chains | | | | |
| RT | of the VH3 subgroup: definitive identification of four heavy chain | | | | |
| RT | hypervariable regions"; | | | | |
| Proc. | Natl. Acad. Sci. U.S.A. 71:845-848(1974). | | | | |
| CC | -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGSI MYELOMA | | | | |
| CC | PROTEIN. | | | | |
| CC | -1- SIMILARITY: Contains 1 immunoglobulin-like domain. | | | | |
| CC | PIR; A02059; GIH0MS. | | | | |
| DR | HSSP; P01772; 2PB4. | | | | |
| DR | GO; GO:0005576; C:extracellular; NAS. | | | | |
| DR | GO; GO:0003823; F:antigen binding activity; NAS. | | | | |
| DR | GO; GO:0006955; P:immune response; NAS. | | | | |
| DR | InterPro; IPR007110; IG-1like. | | | | |
| DR | InterPro; IPR003066; IG_MHC. | | | | |
| DR | InterPro; IPR003596; IG_V. | | | | |
| DR | Pfam; PF000406; IG_1. | | | | |
| DR | SMART; SM00407; IGv, 1. | | | | |
| DR | PROSITE; PS50835; IG_LIKE; 1. | | | | |
| KW | Immunoglobulin V region. | | | | |
| KW | DOMAIN 1 112 IG-LIKE. | | | | |
| FT | NON TER 117 117 | | | | |
| FT | SEQUENCE 117 AA; 13091 MW; 201DEF0E1E5D39BF CRC64; | | | | |
| Query Match 59.9%; Score 400.5; DB 1; Length 117; | | | | | |
| Best Local Similarity 61.5%; Pred. No. 2.4e-34; | | | | | |
| Matches 75; Conservative 22; Mismatches 20; Indels 5; Gaps 1; | | | | | |
| Qy | 1 QVKLLIEGGGVQPGGSLRVACVAGSFFTRNFGMHWVQAPGKGLIEWAFTIFDASNKGY | | | | 60 |
| Db | 1 EVQLLEISGGGLVQPGGSLRLSCAASGFFSTYVMWVQAPGKGLIEWAFTIFDASNSHF | | | | 60 |
| Qy | 61 GDSVVGRTFVSNDNSKNTLYLQNNGLRADDTAVVYCAREKAVRGISRYNYWMDVWGKGT | | | | 120 |
| Db | 61 ADTVNGRTTISRNDNSKNTLYLQNNGLRADDTAVVYCAKGVSA-----QPTVQGFVDVWGKGT | | | | 115 |
| Qy | 121 VT 122 | | | | |
| Db | 116 VT 117 | | | | |

| ID | HW20 MOUSE | STANDARD; | PRT; | 122 AA. |
|-----------------------|--|--------------------|-------|-------------|
| DT | P01789; | | | |
| DT | 21-JUL-1986 (Rel. 01, Created) | | | |
| DT | 21-JUL-1986 (Rel. 01, Last sequence update) | | | |
| DT | 15-SEP-2003 (Rel. 42, Last annotation update) | | | |
| DE | Ig heavy chain V region M603. | | | |
| OS | Mus musculus (Mouse). | | | |
| OC | Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | |
| OC | Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. | | | |
| OX | NCBI_TaxId=10090; | | | |
| RN | [1] | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RX | MEDLINE=80199926; PubMed=6769593; | | | |
| RA | Early P., Huang H., Davis M., Calame K., Hood L.; | | | |
| RT | "An immunoglobulin heavy chain variable region gene is generated from | | | |
| RL | three segments of DNA: VH, D and JH."; | | | |
| RN | Cell 19:981-992(1980). | | | |
| RP | [2] | | | |
| RX | SEQUENCE OF 1-120. | | | |
| RA | MEDLINE=75017346; PubMed=4213577; | | | |
| RT | Rudikoff S., Potter M.; | | | |
| RL | "Variable region sequence of the heavy chain from a phosphorylcholine | | | |
| RL | binding myeloma protein."; | | | |
| RN | Biochemistry 13:4033-4038(1974). | | | |
| RP | [3] | | | |
| RX | X-RAY CRYSTALLOGRAPHY (3.1 ANGSTROMS) OF FAB FRAGMENT. | | | |
| RA | MEDLINE=75065510; PubMed=4530984; | | | |
| RT | Segal D.M., Padlan E.A., Cohen G.H., Rudikoff S., Potter M., | | | |
| RL | Davies D.R.; | | | |
| RT | "The three-dimensional structure of a phosphorylcholine-binding mouse | | | |
| RL | immunoglobulin Fab and the nature of the antigen binding site."; | | | |
| CC | Proc. Natl. Acad. Sci. U.S.A. 71:4298-4302(1974). | | | |
| CC | -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT | | | |
| CC | BINDS PHOSPHORYLCHOLINE. | | | |
| CC | -1- SIMILARITY: Contains 1 immunoglobulin-like domain. | | | |
| DR | PIR; B90795; AVM563. | | | |
| DR | PDB; 1MCP; 15-JUL-92. | | | |
| DR | PDB; 2MCP; 15-JUL-92. | | | |
| DR | InterPro; IPR007110; 19-1like. | | | |
| DR | InterPro; IPR003006; 19_MHC. | | | |
| DR | InterPro; IPR003596; 19_v. | | | |
| DR | Pfam; PF00047; 19_1. | | | |
| DR | SMART; SM00406; 19v; 1. | | | |
| DR | PROSITE; PS50835; 19_LIKE; 1. | | | |
| FW | XM Immunoglobulin V region; 3D-structure. | | | |
| FW | DOMAIN 1 121 | | | |
| FW | SITE 33 33 | | | |
| FW | SITE 52 52 | | | |
| FW | SITE 7 7 | | | |
| FW | STRAND 11 12 | | | |
| FW | TURN 14 15 | | | |
| FW | STRAND 17 25 | | | |
| FW | TURN 30 31 | | | |
| FW | STRAND 33 39 | | | |
| FW | TURN 41 42 | | | |
| FW | STRAND 46 50 | | | |
| FW | TURN 54 55 | | | |
| FW | STRAND 61 61 | | | |
| FW | TURN 64 69 | | | |
| FW | STRAND 70 75 | | | |
| FW | TURN 76 79 | | | |
| FW | STRAND 80 86 | | | |
| FW | HELIX 90 92 | | | |
| FW | STRAND 94 103 | | | |
| FW | STRAND 107 112 | | | |
| FW | STRAND 116 120 | | | |
| FW | NON TER 122 122 | | | |
| FW | SEQUENCE 122 AA; 13626 MW; BAZC864438B64F0F CRC64; | | | |
| Query Match | 59.9%; | Score 400.5; | DB 1; | Length 122; |
| Best Local Similarity | 61.0%; | Pred. No. 2.5e-34; | | |

Matches 83; Conservative 11; Mismatches 17; Indels 25; Gaps 4;

QY 1 QVLLSEGGGVVOPGSLRVAACVAGTFFNFGHMWRQAPGKLEVAFIWPDASNGK-59
 DB 1 EVKLVEGGGGLVOPGSLRVAACVAGTFFNFGHMWRQAPGKLEVAFIWPDASNGK-56
 QY 60 -----YGDVSKGRFTVSRDNRKNTLYLQMNGLRAEDTAVVYCAEKAIVRIGISRYNY----110
 DB 57 KYTTEYASVAKGRIVRDRDTSQSLIYQMNALRAEDTAIYCA-----NYGST 106
 QY 111 -YMDVWKGTTVTYSS 125
 DB 107 WYEDVWAGTTVTYSS 122

RESULT 11

HW33_MOUSE
 ID HW33_MOUSE STANDARD; PRT; 123 AA.
 AC P01792;
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 RT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Ig heavy chain V region HPCG8.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NC NCBI_TaxID=10090;
 RN (1)
 RP SEQUENCE.
 RX MEDLINE=8197602; PubMed=7231520;
 RA Gearhart P.J., Johnson N.D., Douglas R., Hood L.;
 RT "IgG antibodies to phosphorylcholine exhibit more diversity than
 RT their IGM counterparts";
 RL Nature 251:23-34(1981).
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
 CC BINDS PHOSPHORYLCHOLINE.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
 CC PIR: E93256; AVMSH8.
 DR HSP; P01789; IMCP.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SMO0406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 DR Immunoglobulin V region; Hybridoma.
 FT DOMAIN 1 114 IG-LIKE.
 FT NON_TER 123 123
 SQ SEQUENCE 123 AA; 13879 MW; 4559D3106CAE7D8D CRC64;

Query Match 59.8%; Score 400; DB 1; Length 123;
 Best Local Similarity 64.1%; Pred. No. 2.8e-34;
 Matches 84; Conservative 13; Mismatches 20; Indels 14; Gaps 5;

QY 1 QVLLSEGGGVVOPGSLRVAACVAGTFFNFGHMWRQAPGKLEVAFIWPDASNGK-59
 DB 1 EVKLVEGGGGLVOPGSLRVAACVAGTFFNFGHMWRQAPGKLEVAFIWPDASNGK-56
 QY 60 -----YGDVSKGRFTVSRDNRKNTLYLQMNGLRAEDTAVVYCAEKAIVRIGISRYNYMDV 114
 DB 57 DYTTEYASVAKGRIVRDRDTSQSLIYQMNALRAEDTAIYCA-----YYG-SRY-WYFDV 112
 QY 115 WKGTTVTYSS 125
 DB 113 WAGTTVTYSS 123

RESULT 12

HW33_HUMAN
 ID HW33_HUMAN STANDARD; PRT; 116 AA.
 AC P01781;
 DT 21-JUL-1986 (Rel. 01, Created)
 RT 21-JUL-1986 (Rel. 01, Last sequence update)
 RL Proc. Natl. Acad. Sci. U.S.A. 77:6561-6565(1980).

DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Ig heavy chain V-II region GAL.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NC NCBI_TaxID=9606;
 RN (1)
 RP SEQUENCE.
 RX MEDLINE=75059123; PubMed=4803843;
 RA Watanabe S., Barnikol H.U., Horn J., Bertram J., Hilschmann N.;
 RT "The primary structure of a monoclonal IgM-immunoglobulin
 RT (macroglobulin Gal.), II: the amino acid sequence of the H-chain (mu-
 RT type), subgroup H III. Architecture of the complete IgM-molecule";
 RL Hoppe-Seyler's Z. Physiol. Chem. 354:1505-1509(1973).
 RN (2)
 RP REVISION TO 28-33.

RA Hilschmann N.;
 RL Submitted (JUN-1975) to the PIR data bank.
 CC -1- MISCELLANEOUS: THIS MU CHAIN WAS ISOLATED FROM A WALDENSTROM'S
 CC MACROGLOBULIN.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
 CC PIR: A02064; MATHGL.
 DR HSP; P01772; 2PB4.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding activity; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_MHC.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SMO0406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 DR Immunoglobulin V region.
 FT DOMAIN 1 112 IG-LIKE.
 FT NON_TER 116 116
 SQ SEQUENCE 116 AA; 12730 MW; 2C67CA9AAAAA1282 CRC64;

Query Match 59.7%; Score 399.5; DB 1; Length 116;
 Best Local Similarity 63.2%; Pred. No. 3e-34;
 Matches 79; Conservative 16; Mismatches 21; Indels 9; Gaps 2;

QY 1 QVLLSEGGGVVOPGSLRVAACVAGTFFNFGHMWRQAPGKLEVAFIWPDASNGK-60
 DB 1 EVKLVEGGGGLVOPGSLRVAACVAGTFFNFGHMWRQAPGKLEVAFIWPDASNGK-56
 QY 61 GDSVSKGRFTVSRDNRKNTLYLQMNGLRAEDTAVVYCAEKAIVRIGISRYNYMDVWKGTT 120
 DB 61 VDSVSKGRFTVSRDNRKNTLYLQMNGLRAEDTAVVYCAEKAIVRIGISRYNYMDVWKGTT 111
 QY 121 VTYSS 125
 DB 112 VTYST 116

RESULT 13

HW33_HUMAN
 ID HW33_HUMAN STANDARD; PRT; 117 AA.
 AC P01764;
 DT 21-JUL-1986 (Rel. 01, Created)
 RT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Ig heavy chain V-III region VH26 precursor.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NC NCBI_TaxID=9606;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=81101090; PubMed=6450418;
 RA Macthysens G., Rabbits T.H.;
 RT "Structure and multiplicity of genes for the human immunoglobulin
 RT heavy chain variable region";
 RL Proc. Natl. Acad. Sci. U.S.A. 77:6561-6565(1980).

CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
 CC at the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.ebi.ac.uk/announcements>
 CC or send an email to license@ebi.ac.uk).

DR EMBL: J00236; AAA5516.1; -
 DR EMBL: M35415; AAA58735.1; -
 DR PIR: A02047; H3H26.
 DR PDB: 1H0J; 23-DEC-99.
 DR Genew: HGNC:5545; IGHV.
 DR GO: GO:0005576; C:extracellular; NAS.
 DR GO: GO:0003823; F:antigen binding activity; NAS.
 DR GO: GO:0006955; P:immune response; NAS.
 DR InterPro: IPR007110; IG-like.
 DR InterPro: IPR003006; IG_MHC.
 DR InterPro: IPR003596; IG_V.
 DR Pfam: PF00047; Ig; 1.
 DR SMART: SM00406; IGV; 1.
 DR PROSITE: PS50835; IG_LIKE; 1.
 DR Immunoglobulin V region; Signal; 3D-structure.
 FT CHAIN 1 19 IG HEAVY CHAIN V-III REGION VH26.
 FT DOMAIN 20 >117 IG-LIKE.
 FT NON_TER 117 117
 SQ SEQUENCE 117 AA; 12582 MW; E826733F1A3CB0F1 CRC64;

Query Match 59.6%; Score 399; DB 1; Length 117;
 Best Local Similarity 75.5%; Pred. No. 3.4e-34;
 Matches 74; Conservative 11; Mismatches 13; Indels 0; Gaps 0;

QY 1 QVLTLESGGCVVPGGSLRVACVAGFTFRNFGMHVWRQAPGKGLFWAFIFDASNKGY 60
 DB 20 EVQLLESGGGLVPGGSLRLSCAASGFTFSYMSWRQAPGKGLEWVAISSGSGSTYY 79

QY 61 GDSVKGKFTVSRNDSKNTLYLQNGLRABDTAVYYCAK 98
 DB 80 GDSVKGKFTVSRNDSKNTLYLQNGLRABDTAVYYCAK 117

RESULT 14
 HV22_MOUSE STANDARD; PRT; 123 AA.
 AC P01791;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Ig heavy chain V region HPCMC.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=8197602; PubMed=7231520;
 RA Gearhart P.J., Johnson N.D., Douglas R., Hood L.;
 RT "IgG antibodies to phosphorylcholine exhibit more diversity than
 RT their IgM counterparts.";
 RL Nature 291:29-34(1981).
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
 CC BINDS PHOSPHORYLCHOLINE.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
 DR PIR: D93256; AVMSH6.
 DR HSSP: P01789; IMCP.
 DR InterPro: IPR007110; IG-like.
 DR InterPro: IPR003006; IG_MHC.
 DR InterPro: IPR003596; IG_V.
 DR Pfam: PF00047; Ig; 1.
 DR SMART: SM00406; IGV; 1.

DR PROSITE; PS50835; IG_LIKE; 1.
 KM Immunoglobulin V region; Hybridoma.
 FT DOMAIN 1 114 IG-LIKE.
 FT NON_TER 123 123
 SQ SEQUENCE 123 AA; 13895 MW; 81361892ECBF7000 CRC64;

Query Match 59.6%; Score 399; DB 1; Length 123;
 Best Local Similarity 61.2%; Pred. No. 3.5e-34;
 Matches 82; Conservative 13; Mismatches 19; Indels 20; Gaps 4;

QY 1 QVLTLESGGCVVPGGSLRVACVAGFTFRNFGMHVWRQAPGKGLFWAFIFDASNKGY 59
 DB 1 EVQLVSGGGLVPGGSLRLSCAASGFTFSDFMEWVRQPPGKRLFWIA-----ASHKKN 56

QY 60 -----YGDSVKGKFTVSRNDSKNTLYLQNGLRABDTAVYYCAKREAVAGISRYN---Y 111
 DB 57 DYTTESASVKGKFTVSRNDSKNTLYLQNGLRABDTAVYYCAKREAVAGISRYN---Y 109

QY 112 MDVWKGKFTVTVSS 125
 DB 110 FDVWKGKFTVTVSS 123

RESULT 15
 HV23_HUMAN STANDARD; PRT; 114 AA.
 AC P01763;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Ig heavy chain V-III region WEA.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=83273707; PubMed=6410398;
 RA Goni F., Frangione B.;
 RT "Amino acid sequence of the Fv region of a human monoclonal IgM
 RT (protein WEA) with antibody activity against 3,4-pyruvylated
 RT galactose in Klebsiella polysaccharides K30 and K33.";
 RL Proc. Natl. Acad. Sci. U.S.A. 80:4837-4841(1983).
 CC -1- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM A MONOCLONAL ANTIBODY
 CC AGAINST 3,4-PYRUVYLATED GALACTOSE AND ISOLATED FROM A PATIENT WITH
 CC WALDENSTROM'S MACROGLOBULINEMIA.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
 DR PIR: A02046; M3HWE.
 DR HSSP: P01772; 2F84.
 DR GO: GO:0005576; C:extracellular; NAS.
 DR GO: GO:0003823; F:antigen binding activity; NAS.
 DR GO: GO:0006955; P:immune response; NAS.
 DR InterPro: IPR007110; IG-like.
 DR InterPro: IPR003006; IG_MHC.
 DR InterPro: IPR003596; IG_V.
 DR Pfam: PF00047; Ig; 1.
 DR SMART: SM00406; IGV; 1.
 DR PROSITE: PS50835; IG_LIKE; 1.
 KM Immunoglobulin V region; Pyruvylated carboxylic acid.
 FT DOMAIN 1 112 IG-LIKE.
 FT MOD_RES 1 112 PYRROLIDONE CARBOXYLIC ACID.
 FT NON_TER 114 114
 SQ SEQUENCE 114 AA; 12256 MW; D88294FB418A07B7 CRC64;

Query Match 59.6%; Score 398.5; DB 1; Length 114;
 Best Local Similarity 62.4%; Pred. No. 3.7e-34;
 Matches 78; Conservative 18; Mismatches 18; Indels 11; Gaps 1;

QY 1 QVLTLESGGCVVPGGSLRVACVAGFTFRNFGMHVWRQAPGKGLFWAFIFDASNKGY 60
 DB 1 QVLTLESGGGLVPGGSLRLSCAASGFTFSANDMWRQAPGKGLEWVAISSGSGSTYY 60

QY 61 GDSVKGKFTVSRNDSKNTLYLQNGLRABDTAVYYCAKREAVAGISRYNVDVWKGKFTT 120

Db 61 ADVKGRFTISRNBKSNLYLQMSLRAPDTAVYYCARG-----MLNMGQTL 109

QY 121 VTVSS 125
Db 110 VTVSS 114

Search completed: January 22, 2004, 11:51:48
Job time : 10.8696 secs

| Result | Score | Query | Match | Length | DB | ID | Description |
|--------|-------|-------|-------|--------|--------|--------|--------------|
| No. | | | | | | | |
| 1 | 483 | 72.2 | 113 | 4 | Q9UT90 | Q9U190 | homo sapien |
| 2 | 480.5 | 71.8 | 613 | 4 | Q8WUK1 | Q8WUK1 | homo sapien |
| 3 | 457 | 68.3 | 499 | 4 | Q8NSK4 | Q8NSK4 | homo sapien |
| 4 | 456.5 | 68.2 | 573 | 4 | Q8WU38 | Q8WU38 | homo sapien |
| 5 | 449 | 67.1 | 121 | 4 | Q9UW71 | Q9U171 | homo sapien |
| 6 | 448.5 | 67.0 | 122 | 4 | Q9UW84 | Q9U184 | homo sapien |
| 7 | 446 | 66.7 | 116 | 4 | Q9UI93 | Q9U193 | homo sapien |
| 8 | 445 | 66.2 | 453 | 4 | Q8NCL6 | Q9U193 | homo sapien |
| 9 | 441.5 | 66.0 | 471 | 4 | Q8TC77 | Q8TC77 | homo sapien |
| 10 | 435.5 | 65.1 | 112 | 4 | Q9HCC1 | Q8TC76 | homo sapien |
| 11 | 433.5 | 64.8 | 147 | 4 | Q9Y509 | Q9HCC1 | homo sapien |
| 12 | 431 | 64.4 | 597 | 4 | Q96B89 | Q9Y509 | homo sapien |
| 13 | 424.5 | 63.5 | 473 | 11 | Q9U205 | Q96B89 | mus musculus |
| 14 | 423.5 | 63.3 | 118 | 4 | Q9U192 | Q9U205 | homo sapien |
| 15 | 401.5 | 60.0 | 118 | 4 | Q9U171 | Q9U192 | homo sapien |
| 16 | 398.5 | 59.6 | 494 | 4 | Q96K68 | Q9U171 | homo sapien |

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|----|-------|------|-----|----|--------|
| 15 | 309 | 46.2 | 117 | 11 | Q9QXF0 |
| 16 | 311 | 46.5 | 119 | 5 | Q9GYZ2 |
| 17 | 312.5 | 46.7 | 613 | 11 | Q8VCX7 |
| 18 | 313.5 | 46.9 | 482 | 11 | Q91X92 |
| 19 | 316 | 47.2 | 119 | 4 | Q91U94 |
| 20 | 317.5 | 47.5 | 145 | 11 | Q92AR3 |
| 21 | 327 | 48.9 | 484 | 11 | Q91RA6 |
| 22 | 328.5 | 49.3 | 121 | 11 | Q93NG4 |
| 23 | 332 | 49.6 | 241 | 11 | Q921A6 |
| 24 | 334.5 | 50.0 | 112 | 4 | Q9UGP3 |
| 25 | 335 | 50.0 | 437 | 11 | Q91RA4 |
| 26 | 335 | 50.1 | 125 | 4 | Q91U95 |
| 27 | 337 | 50.4 | 104 | 4 | Q91U87 |
| 28 | 361 | 54.0 | 131 | 4 | Q91U88 |
| 29 | 351.5 | 52.5 | 124 | 6 | Q9N0M6 |
| 30 | 350.5 | 52.4 | 124 | 6 | Q9N0M4 |
| 31 | 342.5 | 51.2 | 159 | 4 | Q96OS0 |
| 32 | 338.5 | 50.6 | 500 | 4 | Q9BRV0 |
| 33 | 335 | 50.1 | 125 | 4 | Q91U95 |
| 34 | 334.5 | 50.0 | 124 | 4 | Q91U92 |
| 35 | 334.5 | 50.0 | 437 | 11 | Q91RA4 |
| 36 | 332 | 49.6 | 112 | 4 | Q9UGP3 |
| 37 | 331.5 | 49.6 | 241 | 11 | Q921A6 |
| 38 | 328.5 | 49.3 | 121 | 11 | Q93NG4 |
| 39 | 327 | 48.9 | 484 | 11 | Q91RA6 |
| 40 | 317.5 | 47.5 | 145 | 11 | Q92AR3 |
| 41 | 316 | 47.2 | 119 | 4 | Q91U94 |
| 42 | 313.5 | 46.9 | 482 | 11 | Q91X92 |
| 43 | 312.5 | 46.7 | 613 | 11 | Q8VCX7 |
| 44 | 311 | 46.5 | 119 | 5 | Q9GYZ2 |
| 45 | 309 | 46.2 | 117 | 11 | Q9QXF0 |

ALIGNMENTS

RESULT 1

| | | | | | |
|----|--------|--------------|------|-----|----|
| ID | Q9UL90 | PRELIMINARY; | PRT; | 113 | AA |
|----|--------|--------------|------|-----|----|

DT 01-MAY-2000 (Tremblay, 13, Created)

DT 01-MAR-2003 (Tremblay, 23, Last annotation update)

DE (Fragment).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

NCBI_TaxID=9606;

| RP | SEQUENCE FROM N.A. |
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RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.

RT "Myosin-reactive autoantibodies in rheumatic carditis and normal

RL Clin. Immunol. Immunopathol. 87:184-192 (1998).

DR HSP; P01772; 2FB4.

DR InterPro; IPR003006; Ig_MHC.

DR Pfam; PF00047; ig; 1.

DR PROSITE; PS50835; IG_LIKE; 1.

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| FT | NON_TER | 113 | 113 |
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Best Local Similarity 72.0%; Pred. No. 2.5e-43;
Watched 00; Generated 14; Missed 0; Total 14; Correct 1

[illegible]

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Db 1 EVOLVESGGGVPGGSLRLSCAASGFTFSYGVHWRQAPGKGLWVAIFRYDGSNKYY 60
QY 61 GDSYKGRFTVSRDMSKNTLYIQMNGLRAPDPAVYYCAKRAVGRISRYNYMDVWGKGT 120
Db 61 ADSYKGRFTISRDNKNTLYIQMNSLRAPDPAVYYCAKD-----LNYWGQGT 108
QY 121 VTWSS 125
Db 109 VTWSS 113

RESULT 2
Q8WUK1 PRELIMINARY; PRT; 613 AA.
AC Q8WUK1 01-MAR-2002 (Tremblrel. 20, Created)
DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Strauberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC020240; AAH20240.1; -.
DR InterPro; IPR007110; IG_1ike.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG_5.
DR SMART; SM00406; IGV_1.
DR PROSITE; PS50835; IG_LIKE; 5.
DR PROSITE; PS00290; IG_MHC; 3.
KW Hypothetical protein.
SQ SEQUENCE 613 AA; 67296 MW; 60C7F5950671E315 CRC64;

Query Match 71.8%; Score 480.5; DB 4; Length 613;
Best Local Similarity 72.8%; Pred. No. 3.7e-42;
Matches 91; Conservative 15; Mismatches 14; Indels 5; Gaps 2;

QY 1 QVLLSGGGVPGGSLRVACVAGSFTFRNFGMHWRQAPGKGLWVAIFMPDASNKGY 60
Db 20 QVQLVESGGGVQPERSLRLSCAASGFTFSYGVHWRQAPGKGLWVAIVSYGSNKYY 79
QY 61 GDSYKGRFTVSRDMSKNTLYIQMNGLRAPDPAVYYCAKRAVGRISRYNYMDVWGKGT 120
Db 80 ADSYKGRFTISRDNKNTLYIQMNSLRAPDPAVYYCAKDWG-EGVETP---DIWGQGT 134
QY 121 VTWSS 125
Db 135 VTWSS 139

RESULT 3
Q8NSK4 PRELIMINARY; PRT; 499 AA.
AC Q8NSK4 01-OCT-2002 (Tremblrel. 22, Created)
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RA Strauberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
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DR EMBL; BC032249; AAH32249.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG_1ike.
DR InterPro; IPR003597; IG_CL.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG_4.
DR SMART; SM00409; IGV_4.
DR SMART; SM00407; IGV_2.
DR SMART; SM00406; IGV_1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 499 AA; 53376 MW; 93A5C89582054F32 CRC64;

Query Match 68.3%; Score 457; DB 4; Length 499;
Best Local Similarity 68.8%; Pred. No. 8.8e-40;
Matches 87; Conservative 16; Mismatches 22; Indels 2; Gaps 1;

QY 1 QVLLSGGGVPGGSLRVACVAGSFTFRNFGMHWRQAPGKGLWVAIFMPDASNKGY 60
Db 20 EVOLVESGGGVPGGSLRLSCATSGFTPDGASVWRQAPGKGLWVSIINNGSTNY 79
QY 61 GDSYKGRFTVSRDMSKNTLYIQMNGLRAPDPAVYYCAKRAVGRISRYNYMDVWGK 118
Db 80 ADSYKGRFTISRDNKNTLYIQMNSLRAPDPAVYYCAKPGSGSGSCLGYMDVWGK 139
QY 119 TTYTVSS 125
Db 140 TTYTVSS 146

RESULT 4
Q8WU38 PRELIMINARY; PRT; 573 AA.
AC Q8WU38 01-MAR-2002 (Tremblrel. 20, Created)
DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Strauberg R.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC021276; AAH21276.1; -.
DR InterPro; IPR007110; IG_1ike.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG_4.
DR SMART; SM00406; IGV_1.
DR PROSITE; PS50835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; 2.
KW Hypothetical protein.
SQ SEQUENCE 573 AA; 62967 MW; FD072344033AC530 CRC64;

Query Match 68.2%; Score 456.5; DB 4; Length 573;
Best Local Similarity 68.8%; Pred. No. 1.2e-39;
Matches 86; Conservative 20; Mismatches 18; Indels 1; Gaps 1;

QY 1 QVLLSGGGVPGGSLRVACVAGSFTFRNFGMHWRQAPGKGLWVAIFMPDASNKGY 60
Db 20 EVOLVESGGGVPGGSLRLSCAASGFTPDPAVYYCAKRAVGRISRYNYMDVWGKGT 79
QY 61 GDSYKGRFTVSRDMSKNTLYIQMNGLRAPDPAVYYCAKRAVGRISRYNYMDVWGKGT 120
Db 80 ADSYKGRFTISRDNKNTLYIQMNSLRAPDPAVYYCAKSGSGSYTG-YIYGMDVWGKGT 138
QY 121 VTWSS 125
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[illegible]

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RT      fetus " ;
RL      Clin. Immunol. Immunopathol. 87:184-192(1998).
DR      EMBL; AF035030; AAD56266.1; -.
DR      HSSP; P01772; 2FB4.
DR      InterPro; IPR007110; IG_1like.
DR      InterPro; IPR003006; IG_MHC.
DR      InterPro; IPR003596; IG_V.
DR      Pfam; PF00047; Ig_1.
DR      SMART; SM00406; IGV; 1.
DR      PROSITE; PS50835; IG_LIKE; 1.
FT      NON TER
FT      NON TER
SQ      SEQUENCE   122 AA;  13579 MW;  36054D41366545B8 CRC64;

Query Match                               67.0% Score 448.5; DB 4; Length 122;
Best Local Similarity                     69.6%; Pred. No. 1.2e-39;
Matches    87; Conservative    13; Mismatches   22; Indels     3; Gaps     1

OY      1 QVLLSEGGGVQPGSGSLRVACVSGFTRNFGMHVWROAPGKGLEWVAFIWPDASNKGYG 60
       :|::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB      1 EVQLVESGGGVQPPRSRLRLSCAASGFITSSVAMHVRAQPGKGLEWVAISNDGSNKFY 60
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OY      61 GDSVYGRFTVSRDNSKNLTLYIQMNGLRADPAVYYCAREKAARGISRNYNMDVMWGKTT 120
DB      61 ADSVYGRFTTIRDNSKNMMDLMNSLRADPAVYYCAEDERGLVT---YFDYMGCGTL 117
       |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
OY      121 VTASS 125
DB      118 VTVSS 122

RESULT 7
OY      ID O9UL93 PRELIMINARY; PRT; 116 AA.
O9UL93
ID      AC O9UL93;
DT      01-MAY-2000 (TREMBLrel. 13, Created)
DT      01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE      01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE      Myosin-reactive immunoglobulin heavy chain variable region
        (Fragment).
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX      NCBI_TaxID=9606;
       [1]
RN      SEQUENCE FROM N.A.
RP      MEDLINE=98277139; PubMed=9614934;
RX      Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA      Young D.C.;
SA      "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT      fetus.";
RL      Clin. Immunol. Immunopathol. 87:184-192(1998).
DR      EMBL; AF035021; AAD56257.1; -.
DR      HSSP; P01772; 2FB4.
DR      InterPro; IPR007110; IG_1like.
DR      InterPro; IPR003006; IG_MHC.
DR      InterPro; IPR003596; IG_V.
DR      Pfam; PF00047; Ig_1.
DR      SMART; SM00406; IGV; 1.
DR      PROSITE; PS50835; IG_LIKE; 1.
FT      NON TER
FT      NON TER
SQ      SEQUENCE   116 AA;  12434 MW;  ODA0348154DD6061 CRC64;

Query Match                               66.7% Score 446; DB 4; Length 116;
Best Local Similarity                       70.2%; Pred. No. 2.1e-39;
Matches    87; Conservative    12; Mismatches   17; Indels     8; Gaps     2

OY      2 VKLLSEGGGVQPGSGSLRVACVSGFTRNFGMHVWROAPGKGLEWVAFIWPDASNKGYG 61
       :|::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB      1 VQLVESGGGVQPPRSRLRLSCAASGFITSSVAMHVRAQPGKGLEWVAISYDGNKKYA 60
       ::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

OY      62 DSVMGRFTVSRDNSKNLTLYIQMNGLRADPAVYYCAREKAARGISRNYNMDVMWGKTTV 121

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Db 61 DSVKGRFTIRSDNSKNTLYLQWNGSLRAEDTAVYYCA---GGGGG-----LGYWGQSTLV 112
QY 122 TVSS 125
Db 113 TVSS 116

RESULT 8
Q8NCL6 PRELIMINARY; PRT; 493 AA.
AC Q8NCL6;
DT 01-OCT-2002 (TREMblrel. 22, Created)
DT 01-OCT-2002 (TREMblrel. 22, Last sequence update)
DT 01-MAR-2003 (TREMblrel. 23, Last annotation update)
DE Hypothetical protein FLJ90170.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;

[1]
SEQUENCE FROM N.A.
RC TISSUE=Mammary gland;
RA Isegai T., Oca T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama T.,
RA Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y., Saito K.,
RA Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahari K.,
RA Masuno Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N.,
RA Hattori A., Okumura K., Iwayanagi T., Nimohi Y. K.;
RT "NEDO human cDNA sequencing project.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK074651; BAC1114.1; -.
DR InterPro; IPR003599; IG_1ike.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003597; IG_c1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG_4.
DR SMART; SM00407; IGc1; 2.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 1.
KM Hypothetical protein.
SQ
SEQUENCE 493 AA; 53224 MW; 12ECD7E094777101 CRC64;

Query Match 66.2%; Score 443; DB 4; Length 493;
Best Local Similarity 67.2%; Pred. No. 2.6e-38;
Matches 84; Conservative 16; Mismatches 21; Indels 4; Gaps 2;
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OX NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Strausberg R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC024289; AAH24289.1; -.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG_4.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 2.
KM Hypothetical protein.
SQ
SEQUENCE 471 AA; 51791 MW; 388F7F4CF58660E CRC64;

Query Match 66.0%; Score 441.5; DB 4; Length 471;
Best Local Similarity 66.4%; Pred. No. 3.5e-38;
Matches 83; Conservative 23; Mismatches 16; Indels 3; Gaps 2;
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QY 1 QVLTLSGGGVNPGGSLRACVAGSFTFRNFGMHVWROAPGKLEWVAFIWFDAKNGY 60
Db 20 EVQLVESGGGLVPRGSLRSCAASGFTFSYSMHWROAPGKLEWVSMSSSTIYY 79
QY 61 GDSVKGFTVSRDNSKNTLYLQWNGSLRAEDTAVYYCAREKAVRGISRYNYMDVGKGT 120
Db 80 ADSVKGFTVSRDNSKNTLYLQWNGSLRAEDTAVYYCARD--LRLQLTNY-WYFDLMGKGL 136
QY 121 TVSS 125
Db 137 TVSS 141

RESULT 10
Q9HCCI PRELIMINARY; PRT; 112 AA.
AC Q9HCCI;
DT 01-MAR-2001 (TREMblrel. 16, Created)
DT 01-MAR-2001 (TREMblrel. 16, Last sequence update)
DT 01-MAR-2003 (TREMblrel. 23, Last annotation update)
DE Single chain Fv (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;

[1]
SEQUENCE FROM N.A.
RA Kikuchi M., Takeda C., Teujimoto Y., Aada S., Nagata K.;
RT "An antibody fragment2A3 specific for native lysozyme: isolation from a
human synthetic phage display library and characterization.";
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB049915; BAB16829.1; -.
DR HSP; P01772; 2F84.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG_1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 1
SQ
SEQUENCE 112 AA; 12243 MW; 24FLA45EC3B84788 CRC64;

Query Match 65.1%; Score 435.5; DB 4; Length 112;
Best Local Similarity 66.1%; Pred. No. 2.5e-38;
Matches 80; Conservative 18; Mismatches 14; Indels 9; Gaps 1;
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Db 61 ADGVKGRFTISRDNKNTLYLQNMNSLRADTAIVYCAKRR-----YALDYMGGTL 111
 QY 121 V 121
 Db 112 V 112

RESULT 11

Q9Y509 PRELIMINARY; PRT; 147 AA.

AC Q9Y509; PRELIMINARY; PRT; 147 AA.
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Vh3 protein (Fragment).
 GN Vh3.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 ON NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96071149; PubMed=7475288;
 RA Cao J., Vescio R.A., Rettig M.B., Hong C.H., Kim A., Lee J.C.,
 RA Lichtenstein A.R., Berenson J.R.;
 RT "A CD10-positive subset of malignant cells is identified in multiple
 RT myeloma using PCR with patient-specific immunoglobulin gene primers."
 RL Leukemia 9:1948-1953(1995).
 DR EMBL; S80860; AAD14339.1; -.
 DR HSSP; P01772; 2FB4.
 DR InterPro: IPR007110; I9-like.
 DR InterPro: IPR003006; I9-like.
 DR InterPro: IPR003596; I9-like.
 DR Pfam; PF00047; I9; 1.
 DR SMART; SM00406; I9; 1.
 DR PROSITE; PS50835; I9-like; 1.
 DR SMART; SM00406; I9; 1.
 DR PROSITE; PS50835; I9-like; 1.
 FT NON TER
 SQ SEQUENCE 147 AA; 15768 MW; 8489FCMAA7BC925C CRC64;

Query Match 64.8%; Score 433.5; DB 4; Length 147;
 Best Local Similarity 66.7%; Pred. No. 5.8e-38;
 Matches 84; Conservative 13; Mismatches 28; Indels 1; Gaps 1;

QY 1 QVTLSSGGGVQPGSLRVACVAGSFTFRNFGMHVROAPGKGLFWAFIWFDAANKGY 60
 Db 1 QVHLVSSGGGVQPGSLRVACVAGSFTFRNFGMHVROAPGKGLFWAFIWFDAANKGY 60
 QY 61 GDSVKGRTVSRDNRKNTLYLQNMNSLRADTAIVYCAKRR-KAVRGISRYNYVMDVMGKGT 119
 Db 61 AGSVKGRFTISRDNKNTLYLQNMNSLRADTAIVYCAKRR-KAVRGISRYNYVMDVMGKGT 120
 QY 120 TVTVSS 125
 Db 121 LVTVSS 126

RESULT 12

Q96BB9 PRELIMINARY; PRT; 597 AA.

AC Q96BB9; PRELIMINARY; PRT; 597 AA.
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 ON NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=B-cell;
 RA Strausberg R.;

RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC015760; AA115760.1; -.
 DR InterPro: IPR007110; I9-like.
 DR InterPro: IPR003006; I9-like.
 DR InterPro: IPR003596; I9-like.
 DR Pfam; PF00047; I9; 5.
 DR SMART; SM00406; I9; 1.
 DR PROSITE; PS50835; I9-like; 5.
 DR PROSITE; PS00290; I9-like; 3.
 KW Hypothetical protein.
 SQ SEQUENCE 597 AA; 65039 MW; 4FCA3AD8E6CE263D9 CRC64;

Query Match 64.4%; Score 431; DB 4; Length 597;
 Best Local Similarity 66.1%; Pred. No. 6.1e-37;
 Matches 84; Conservative 17; Mismatches 22; Indels 4; Gaps 2;

QY 1 QVTLSSGGGVQPGSLRVACVAGSFTFRNFGMHVROAPGKGLFWAFIWFDAANKGY 60
 Db 20 EVQLVSSGGGLVQPGSLRVACVAGSFTFRNFGMHVROAPGKGLFWAFIWFDAANKGY 79
 QY 61 GDSVKGRTVSRDNRKNTLYLQNMNSLRADTAIVYCAKRR-KAVRGISRYNYVMDVMGKGT 118
 Db 80 ADGVKGRFTISRDNKNTLYLQNMNSLRADTAIVYCAKRR-KAVRGISRYNYVMDVMGKGT 137
 QY 119 TVTVSS 125
 Db 138 LVTVSS 144

RESULT 13

Q91205 PRELIMINARY; PRT; 473 AA.

AC Q91205; PRELIMINARY; PRT; 473 AA.
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Hypothetical 51.9 kDa protein.
 GN A0044919.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 ON NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.

RA Strausberg R.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC010327; AA10327.1; -.
 DR MGI; MGI:2144967; A0044919.
 DR InterPro: IPR000345; CytC_heme_bind.
 DR InterPro: IPR007110; I9-like.
 DR InterPro: IPR003006; I9-like.
 DR InterPro: IPR003596; I9-like.
 DR Pfam; PF00047; I9; 3.
 DR SMART; SM00406; I9; 1.
 DR PROSITE; PS00190; CYTOCHROME C; 1.
 DR PROSITE; PS50835; I9-like; 4.
 DR PROSITE; PS00290; I9-like; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 473 AA; 51946 MW; CF625F008932AF12 CRC64;

Query Match 63.5%; Score 424.5; DB 11; Length 473;
 Best Local Similarity 63.2%; Pred. No. 2.2e-36;
 Matches 79; Conservative 22; Mismatches 17; Indels 7; Gaps 1;

QY 1 QVTLSSGGGVQPGSLRVACVAGSFTFRNFGMHVROAPGKGLFWAFIWFDAANKGY 60
 Db 20 EVQLVSSGGGLVQPGSLRVACVAGSFTFRNFGMHVROAPGKGLFWAFIWFDAANKGY 79
 QY 61 GDSVKGRTVSRDNRKNTLYLQNMNSLRADTAIVYCAKRR-KAVRGISRYNYVMDVMGKGT 120
 Db 80 ADGVKGRFTISRDNKNTLYLQNMNSLRADTAIVYCAKRR-KAVRGISRYNYVMDVMGKGT 132
 QY 121 TVTVSS 125

Db 133 ITVSS 137

RESULT 14

Q9UL91 PRELIMINARY; PRT; 118 AA.

DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAY-2003 (TREMBlrel. 23, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region (Fragment).

OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_TaxID=9606;

RT fetus."

RA Young, D.C.;

RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus."

RL Clin. Immunol. Immunopathol. 87:184-192(1998).

DR HSSP; P01772; 2FB4.

DR InterPro; IPR007110; Ig_1like.

DR InterPro; IPR003006; Ig_MHC.

DR InterPro; IPR003596; Ig_V.

DR Pfam; PF00047; Ig; 1.

DR SMART; SM00406; IGV; 1.

DR PROSITE; PSS0835; IG_LIKE; 1.

FT NON_TER 1 118

FT NON_TER 1 118

SQ SEQUENCE 118 AA; 12843 MW; D0633949F2AC149D CRC64;

Query Match 63.3%; Score 423.5; DB 4; Length 118;

Best Local Similarity 64.5%; Pred. No. 5e-37; Mismatches 20; Indels 7; Gaps 1;

Matches 80; Conservative 17; Indels 7; Gaps 1;

QY 1 QVLLSGGGVVOPGGSLRVACVAGFTFRNFGMHVWRAQPGKLEWVAFIWPDASNKGY 60

DB 1 EVQLVSGGGLVPGGSLRLSCAASGFTFSYNNMWRQAPGKLEWVSYSITITTY 60

QY 61 GDSYKGRFTVSRDNSKNTLYIQNGILRAEDTAVYGCAREKAVRGISRYNYVM-DVWGKGT 120

DB 61 ADSYKGRFTISRDNKSLYLQNNSLRAEDTAVYGCAREKAVRGISRYNYVM-DVWGKGT 113

QY 121 TVTVSS 124

DB 114 TVTVSS 117

QY 121 TVTVSS 124

DB 114 TVTVSS 117

QY 121 TVTVSS 124

DB 114 TVTVSS 117

QY 121 TVTVSS 124

DB 114 TVTVSS 117

QY 121 TVTVSS 124

DB 114 TVTVSS 117

QY 121 TVTVSS 124

DB 114 TVTVSS 117

QY 121 TVTVSS 124

DB 114 TVTVSS 117

QY 121 TVTVSS 124

DB 114 TVTVSS 117

QY 121 TVTVSS 124

DB 114 TVTVSS 117

QY 121 TVTVSS 124

DB 114 TVTVSS 117

RT fetus."

RA Young, D.C.;

RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus."

RL Clin. Immunol. Immunopathol. 87:184-192(1998).

DR HSSP; P01772; 2FB4.

DR InterPro; IPR007110; Ig_1like.

DR InterPro; IPR003006; Ig_MHC.

DR InterPro; IPR003596; Ig_V.

DR Pfam; PF00047; Ig; 1.

DR SMART; SM00406; IGV; 1.

DR PROSITE; PSS0835; IG_LIKE; 1.

FT NON_TER 1 118

FT NON_TER 1 118

SQ SEQUENCE 118 AA; 12872 MW; B4D1A5944B2D5CCA CRC64;

Query Match 60.0%; Score 401.5; DB 4; Length 118;

Best Local Similarity 63.5%; Pred. No. 1.1e-34; Mismatches 19; Indels 9; Gaps 3;

Matches 80; Conservative 18; Mismatches 19; Indels 9; Gaps 3;

QY 1 QVLLSGGGVVOPGGSLRVACVAGFTFRNFGMHVWRAQPGKLEWVAFIWPDASNKGY 60

DB 1 EVQLVSGGGLVPGGSLRLSCAASGFTFSYNNMWRQAPGKLEWVSYSITITTY 59

QY 61 GDSYKGRFTVSRDNSKNTLYIQNGILRAEDTAVYGCAREKAVRGISRYNYVM-DVWGKGT 119

DB 60 ADSYKGRFTISRDNKSLYLQNNSLRAEDTAVYGCAREKAVRGISRYNYVM-DVWGKGT 112

QY 120 TVTVSS 125

DB 113 LTVTVSS 118

QY 120 TVTVSS 125

DB 113 LTVTVSS 118

QY 120 TVTVSS 125

DB 113 LTVTVSS 118

QY 120 TVTVSS 125

DB 113 LTVTVSS 118

QY 120 TVTVSS 125

DB 113 LTVTVSS 118

QY 120 TVTVSS 125

DB 113 LTVTVSS 118

QY 120 TVTVSS 125

DB 113 LTVTVSS 118

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DB 113 LTVTVSS 118

QY 120 TVTVSS 125

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QY 120 TVTVSS 125

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QY 120 TVTVSS 125

DB 113 LTVTVSS 118

QY 120 TVTVSS 125

DB 113 LTVTVSS 118

QY 120 TVTVSS 125

DB 113 LTVTVSS 118

QY 120 TVTVSS 125

DB 113 LTVTVSS 118

QY 120 TVTVSS 125

DB 113 LTVTVSS 118

QY 120 TVTVSS 125

DB 113 LTVTVSS 118

QY 120 TVTVSS 125

DB 113 LTVTVSS 118

QY 120 TVTVSS 125

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OM protein - protein search, using SW model

Run on: January 22, 2004, 11:37:35 ; Search time 39.1304 Seconds
(without alignments)
507.043 Million cell updates/sec

Title: US-09-147-443d-58

Perfect score: 669

Sequence: 1 QVTLKSGGSGVQPGSLRV.....SRNYMDWGKGTTVSS 125

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_19Jun03.*
1: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
2: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
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12: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.*
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22: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
24: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|-------------|
| 1 | 669 | 100.0 | 125 | 19 | AAW52232 |
| 2 | 669 | 100.0 | 125 | 19 | AAW52240 |
| 3 | 669 | 100.0 | 125 | 19 | AAW52242 |
| 4 | 623 | 93.1 | 125 | 19 | AAW52234 |
| 5 | 615 | 91.9 | 125 | 19 | AAW52236 |
| 6 | 615 | 91.9 | 125 | 19 | AAW52226 |
| 7 | 611 | 91.3 | 125 | 19 | AAW52222 |
| 8 | 600.5 | 89.8 | 126 | 19 | AAW52228 |
| 9 | 590 | 88.2 | 125 | 19 | AAW52218 |

| | | | | | | |
|----|-------|------|-----|----|----------|--------------------|
| 10 | 575.5 | 86.0 | 126 | 19 | AAW52220 | Antibody LD1-117-V |
| 11 | 575 | 85.9 | 125 | 19 | AAW52212 | Antibody LD1-40-VH |
| 12 | 569 | 85.1 | 125 | 19 | AAW52230 | Antibody LD2-11-VH |
| 13 | 569 | 85.1 | 125 | 19 | AAW52224 | Antibody LD2-4-VH |
| 14 | 569 | 85.1 | 125 | 19 | AAW52216 | Antibody LD1-84-VH |
| 15 | 564 | 84.3 | 125 | 19 | AAW52214 | Antibody LD1-52-VH |
| 16 | 543.5 | 81.2 | 126 | 22 | AAW52210 | Human anti-Rh(D) |
| 17 | 543 | 81.2 | 125 | 22 | AAW52208 | Human anti-Rh(D) |
| 18 | 543 | 81.2 | 125 | 22 | AAW52206 | Human anti-Rh(D) |
| 19 | 543 | 81.2 | 125 | 22 | AAW52204 | Human anti-Rh(D) |
| 20 | 543 | 81.2 | 125 | 22 | AAW52202 | Human anti-Rh(D) |
| 21 | 542.5 | 81.1 | 126 | 22 | AAW52200 | Human anti-Rh(D) |
| 22 | 541.5 | 80.9 | 126 | 22 | AAW52198 | Human anti-Rh(D) |
| 23 | 541.5 | 80.9 | 126 | 22 | AAW52196 | Human anti-Rh(D) |
| 24 | 541.5 | 80.9 | 126 | 22 | AAW52194 | Human anti-Rh(D) |
| 25 | 541.5 | 80.9 | 126 | 22 | AAW52192 | Human anti-Rh(D) |
| 26 | 539.5 | 80.6 | 126 | 22 | AAW52190 | Human anti-Rh(D) |
| 27 | 535 | 80.0 | 125 | 22 | AAW52188 | Human anti-Rh(D) |
| 28 | 533 | 79.7 | 127 | 22 | AAW52186 | Human anti-Rh(D) |
| 29 | 530 | 79.2 | 127 | 22 | AAW52184 | Human anti-Rh(D) |
| 30 | 528 | 78.9 | 125 | 22 | AAW52182 | Human anti-Rh(D) |
| 31 | 528 | 78.9 | 125 | 22 | AAW52180 | Human anti-Rh(D) |
| 32 | 527 | 78.8 | 125 | 22 | AAW52178 | Human anti-Rh(D) |
| 33 | 526.5 | 78.7 | 126 | 22 | AAW52176 | Human anti-Rh(D) |
| 34 | 524 | 78.3 | 127 | 22 | AAW52174 | Human anti-Rh(D) |
| 35 | 522.5 | 78.1 | 128 | 19 | AAW52238 | Human anti-Rh(D) |
| 36 | 520.5 | 77.8 | 126 | 22 | AAW52236 | Human anti-Rh(D) |
| 37 | 519 | 77.6 | 127 | 22 | AAW52234 | Human anti-Rh(D) |
| 38 | 518.5 | 77.5 | 126 | 22 | AAW52232 | Human anti-Rh(D) |
| 39 | 518.5 | 77.5 | 126 | 22 | AAW52230 | Human anti-Rh(D) |
| 40 | 517.5 | 77.4 | 126 | 22 | AAW52228 | Human anti-Rh(D) |
| 41 | 517.5 | 77.4 | 143 | 21 | AAW52226 | Human anti-Rh(D) |
| 42 | 517.5 | 77.4 | 143 | 21 | AAW52224 | Human anti-Rh(D) |
| 43 | 516 | 77.1 | 146 | 23 | AAW52222 | Human anti-Rh(D) |
| 44 | 512.5 | 76.6 | 147 | 22 | AAW52220 | Human anti-Rh(D) |
| 45 | 510.5 | 76.3 | 143 | 21 | AAW52218 | Human anti-Rh(D) |

ALIGNMENTS

RESULT 1
AAW52232 standard; Protein; 125 AA.
ID AAW52232:
AC AAW52232:
XX
DT 12-JUN-1998 (first entry)
XX
DE Antibody LD2-14-VH chain sequence.
XX
KW Antibody; variable heavy chain; VH chain; variable light chain; VL chain; Rhesus D antigen; anti-Rhesus D immunoglobulin; HDN therapy;
KW Idiopathic thrombocytopenic purpura; haemolytic disease of the newborn.
XX
OS Homo sapiens.
XX
PN WO9749809-A1.
XX
PD 31-DEC-1997.
XX
PF 20-JUN-1997; 97WO-EP03253.
XX
PR 24-JUN-1996; 96EP-0810421.
XX
(ROTK-) ROTKREUZSTIFTUNG ZENT LAB BLUTSPENDE.
XX
PI Amstutz H, Imboden M, Miescher S, Morell A, Stadler B;
PI Vogel M;
DR WFI, 1998-077173/07.
DR N-PSDB; AAV19756.
XX

PT New Rhesus D antigen binding poly:peptide(s) - used to neutralise
PT Rhesus D antigen in therapy, e.g. for treating idiopathic
PT thrombocytopenic purpura
PS Claim 1, Fig 11A; 68pp; English.
XX
XX This sequence is the antibody LD2-14-VH chain sequence, which is a
CC polypeptide of the invention. The polypeptides are capable of forming
CC antigen binding structures with specificity for Rhesus D antigens which
CC include Rhesus D-specific CDR 1, CDR 2, and CDR 3 regions of pairs of
CC variable heavy (VH) and variable light (VL) chain sequences. The
CC antibodies are active against the Rhesus D antigen. They can be used for
CC treating disorders which would benefit from anti-Rhesus D immunoglobulin,
CC e.g. idiopathic thrombocytopenic purpura. They can also be used for the
CC protection of Rhesus negative women before or immediately after the birth
CC of a Rhesus positive child to prevent haemolytic disease of the newborn
CC (HDN) in subsequent pregnancies. In addition, anti-Rhesus D
CC immunoglobulin can be used after mistransfusions of Rhesus positive blood
CC to Rhesus negative recipients in order to prevent sensitisation to the
CC Rhesus D antigen. The products can also be used as diagnostic reagents.
XX
SQ Sequence 125 AA;
Query Match 100.0%; Score 669; DB 19; Length 125;
Best Local Similarity 100.0%; Pred. No. 5.1e-55;
Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QVLTLSGGGVVPGGSLRVACVAGSFTFRNFGMHVROAPGKLEWVAFIWPDSNKGK 60
DB 1 QVLTLSGGGVVPGGSLRVACVAGSFTFRNFGMHVROAPGKLEWVAFIWPDSNKGK 60
QY 61 GDSVKGRFTVSRDNSKNTLYLQNNGLRAEDTAVYYCAREKAVRGISRYNYMDVWGKTT 120
DB 61 GDSVKGRFTVSRDNSKNTLYLQNNGLRAEDTAVYYCAREKAVRGISRYNYMDVWGKTT 120
QY 121 VTWSS 125
DB 121 VTWSS 125
RESULT 2
AAW52240
ID AAW52240 standard; Protein; 125 AA.
XX
AC AAW52240;
XX
DT 12-JUN-1998 (first entry)
XX
DE Antibody LD1/2-6-3-VH chain sequence.
XX
KM Antibody; variable heavy chain; VH chain; variable light chain; VL chain;
KM Rhesus D antigen; anti-Rhesus D immunoglobulin; HDN; therapy;
KM idiopathic thrombocytopenic purpura; haemolytic disease of the newborn.
XX
OS Homo sapiens.
XX
EN WO9749809-A1.
XX
PD 31-DEC-1997.
XX
PF 20-JUN-1997; 97WO-EP03253.
XX
PR 24-JUN-1996; 96EP-0810421.
XX
PA (ROTK-) ROTKREUZSTIFTUNG ZENT LAB BLUTSPENDE.
XX
PI Amstutz H, Imboden M, Miescher S, Morell A, Stadler B;
PI Vogel M;
XX
XX WPI; 1998-077173/07.
DR N-PSDB; AAV19764.
XX
PT New Rhesus D antigen binding poly:peptide(s) - used to neutralise

PT Rhesus D antigen in therapy, e.g. for treating idiopathic
PT thrombocytopenic purpura
PS Claim 1, Fig 15A; 68pp; English.
XX
XX This sequence is the antibody LD1/2-6-3-VH chain sequence, which is a
CC polypeptide of the invention. The polypeptides are capable of forming
CC antigen binding structures with specificity for Rhesus D antigens which
CC include Rhesus D-specific CDR 1, CDR 2, and CDR 3 regions of pairs of
CC variable heavy (VH) and variable light (VL) chain sequences. The
CC antibodies are active against the Rhesus D antigen. They can be used for
CC treating disorders which would benefit from anti-Rhesus D immunoglobulin,
CC e.g. idiopathic thrombocytopenic purpura. They can also be used for the
CC protection of Rhesus negative women before or immediately after the birth
CC of a Rhesus positive child to prevent haemolytic disease of the newborn
CC (HDN) in subsequent pregnancies. In addition, anti-Rhesus D
CC immunoglobulin can be used after mistransfusions of Rhesus positive blood
CC to Rhesus negative recipients in order to prevent sensitisation to the
CC Rhesus D antigen. The products can also be used as diagnostic reagents.
XX
SQ Sequence 125 AA;
Query Match 100.0%; Score 669; DB 19; Length 125;
Best Local Similarity 100.0%; Pred. No. 5.1e-55;
Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QVLTLSGGGVVPGGSLRVACVAGSFTFRNFGMHVROAPGKLEWVAFIWPDSNKGK 60
DB 1 QVLTLSGGGVVPGGSLRVACVAGSFTFRNFGMHVROAPGKLEWVAFIWPDSNKGK 60
QY 61 GDSVKGRFTVSRDNSKNTLYLQNNGLRAEDTAVYYCAREKAVRGISRYNYMDVWGKTT 120
DB 61 GDSVKGRFTVSRDNSKNTLYLQNNGLRAEDTAVYYCAREKAVRGISRYNYMDVWGKTT 120
QY 121 VTWSS 125
DB 121 VTWSS 125
RESULT 3
AAW52242
ID AAW52242 standard; Protein; 125 AA.
XX
AC AAW52242;
XX
DT 12-JUN-1998 (first entry)
XX
DE Antibody LD1/2-6-33-VH chain sequence.
XX
KM Antibody; variable heavy chain; VH chain; variable light chain; VL chain;
KM Rhesus D antigen; anti-Rhesus D immunoglobulin; HDN; therapy;
KM idiopathic thrombocytopenic purpura; haemolytic disease of the newborn.
XX
OS Homo sapiens.
XX
EN WO9749809-A1.
XX
PD 31-DEC-1997.
XX
PF 20-JUN-1997; 97WO-EP03253.
XX
PR 24-JUN-1996; 96EP-0810421.
XX
PA (ROTK-) ROTKREUZSTIFTUNG ZENT LAB BLUTSPENDE.
XX
PI Amstutz H, Imboden M, Miescher S, Morell A, Stadler B;
PI Vogel M;
XX
XX WPI; 1998-077173/07.
DR N-PSDB; AAV19766.
XX
PT New Rhesus D antigen binding poly:peptide(s) - used to neutralise
PT Rhesus D antigen in therapy, e.g. for treating idiopathic

PT thrombocytopenic purpura
XX
PS Claim 1, Fig 16A, 68pp; English.
XX
CC This sequence is the antibody LD1/2-6-33-VH chain sequence, which is a
CC polypeptide of the invention. The polypeptides are capable of forming
CC antigen binding structures with specificity for Rhesus D antigens which
CC include Rhesus D-specific CDR 1, CDR 2, and CDR 3 regions of pairs of
CC variable heavy (VH) and variable light (VL) chain sequences. The
CC antibodies are active against the Rhesus D antigen. They can be used for
CC treating disorders which would benefit from anti-Rhesus D immunoglobulin,
CC e.g. idiopathic thrombocytopenic purpura. They can also be used for the
CC protection of Rhesus negative women before or immediately after the birth
CC of a Rhesus positive child to prevent haemolytic disease of the newborn
CC (HDN) in subsequent pregnancies. In addition, anti-Rhesus D
CC immunoglobulin can be used after transfusions of Rhesus positive blood
CC to Rhesus negative recipients in order to prevent sensitisation to the
CC Rhesus D antigen. The products can also be used as diagnostic reagents.
XX
SQ Sequence 125 AA;
Query Match 100.0%; Score 669; DB 19; Length 125;
Best Local Similarity 100.0%; Pred. No. 5, 1e-55;
Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QVLTLESGGGVVPGGSLRVACVAGFTFRNFGMHWVROAPGKGLBWAFFIMFDASNKGY 60
DB 1 QVLTLESGGGVVPGGSLRVACVAGFTFRNFGMHWVROAPGKGLBWAFFIMFDASNKGY 60
QY 61 GDSVKGRFTVSRDNRKNTLYLQWNGLRADDTAVYYCARERKAVRGISRYNYMDWGKGT 120
DB 61 GDSVKGRFTVSRDNRKNTLYLQWNGLRADDTAVYYCARERKAVRGISRYNYMDWGKGT 120
QY 121 VTVSS 125
DB 121 VTVSS 125

RESULT 4
AAM52234
ID AAM52234 standard; Protein; 125 AA.
XX
AC AAM52234;
XX
DT 12-JUN-1998 (first entry)
XX
DE Antibody LD2-17-VH chain sequence.
XX
DE Antibody; variable heavy chain; VH chain; variable light chain; VL chain;
XX Rhesus D antigen; anti-Rhesus D immunoglobulin; HDN; therapy;
XX idiopathic thrombocytopenic purpura; haemolytic disease of the newborn.
XX
OS Homo sapiens.
XX
PN MO9749809-A1.
XX
PD 31-DEC-1997.
XX
PF 20-JUN-1997; 97WO-EP03253.
XX
PR 24-JUN-1996; 96EP-0810421.
XX
PA (ROTK-) ROTKREUZSTIFTUNG ZENT LAB BLUTSPENDE.
XX
PI Amstutz H, Imboden M, Miescher S, Morell A, Stadler B;
XX Vogel M;
XX WPI; 1998-077173/07.
XX N-PSDB; AAV19758.
XX
PT New Rhesus D antigen binding poly:peptide(s) - used to neutralise
PT Rhesus D antigen in therapy, e.g. for treating idiopathic
PT thrombocytopenic purpura

XX
PS Claim 1, Fig 12A, 68pp; English.
XX
CC This sequence is the antibody LD2-17-VH chain sequence, which is a
CC polypeptide of the invention. The polypeptides are capable of forming
CC antigen binding structures with specificity for Rhesus D antigens which
CC include Rhesus D-specific CDR 1, CDR 2, and CDR 3 regions of pairs of
CC variable heavy (VH) and variable light (VL) chain sequences. The
CC antibodies are active against the Rhesus D antigen. They can be used for
CC treating disorders which would benefit from anti-Rhesus D immunoglobulin,
CC e.g. idiopathic thrombocytopenic purpura. They can also be used for the
CC protection of Rhesus negative women before or immediately after the birth
CC of a Rhesus positive child to prevent haemolytic disease of the newborn
CC (HDN) in subsequent pregnancies. In addition, anti-Rhesus D
CC immunoglobulin can be used after transfusions of Rhesus positive blood
CC to Rhesus negative recipients in order to prevent sensitisation to the
CC Rhesus D antigen. The products can also be used as diagnostic reagents.
XX
SQ Sequence 125 AA;
Query Match 93.1%; Score 623; DB 19; Length 125;
Best Local Similarity 91.2%; Pred. No. 1e-50;
Matches 114; Conservative 7; Mismatches 4; Indels 0; Gaps 0;
QY 1 QVLTLESGGGVVPGGSLRVACVAGFTFRNFGMHWVROAPGKGLBWAFFIMFDASNKGY 60
DB 1 QVLTLESGGGVVPGGSLRVACVAGFTFRNFGMHWVROAPGKGLBWAFFIMFDASNKGY 60
QY 61 GDSVKGRFTVSRDNRKNTLYLQWNGLRADDTAVYYCARERKAVRGISRYNYMDWGKGT 120
DB 61 GDSVKGRFTVSRDNRKNTLYLQWNGLRADDTAVYYCARERKAVRGISRYNYMDWGKGT 120
QY 121 VTVSS 125
DB 121 VTVSS 125

RESULT 5
AAM52236
ID AAM52236 standard; Protein; 125 AA.
XX
AC AAM52236;
XX
DT 12-JUN-1998 (first entry)
XX
DE Antibody LD2-20-VH chain sequence.
XX
DE Antibody; variable heavy chain; VH chain; variable light chain; VL chain;
XX Rhesus D antigen; anti-Rhesus D immunoglobulin; HDN; therapy;
XX idiopathic thrombocytopenic purpura; haemolytic disease of the newborn.
XX
OS Homo sapiens.
XX
PN MO9749809-A1.
XX
PD 31-DEC-1997.
XX
PF 20-JUN-1997; 97WO-EP03253.
XX
PR 24-JUN-1996; 96EP-0810421.
XX
PA (ROTK-) ROTKREUZSTIFTUNG ZENT LAB BLUTSPENDE.
XX
PI Amstutz H, Imboden M, Miescher S, Morell A, Stadler B;
XX Vogel M;
XX WPI; 1998-077173/07.
XX N-PSDB; AAV19760.
XX
PT New Rhesus D antigen binding poly:peptide(s) - used to neutralise
PT Rhesus D antigen in therapy, e.g. for treating idiopathic
PT thrombocytopenic purpura

PS Claim 1; Fig 13A; 68bp; English.

XX This sequence is the antibody LD2-20-VH chain sequence, which is a
CC polypeptide of the invention. The polypeptides are capable of forming
CC antigen binding structures with specificity for Rhesus D antigens which
CC include Rhesus D-specific CDR 1, CDR 2, and CDR 3 regions of pairs of
CC variable heavy (VH) and variable light (VL) chain sequences. The
CC antibodies are active against the Rhesus D antigen. They can be used for
CC treating disorders which would benefit from anti-Rhesus D immunoglobulin,
CC e.g. idiopathic thrombocytopenic purpura. They can also be used for the
CC protection of Rhesus negative women before or immediately after the birth
CC of a Rhesus positive child to prevent haemolytic disease of the newborn
CC (HDN) in subsequent pregnancies. In addition, anti-Rhesus D
CC immunoglobulin can be used after mistransfusions of Rhesus positive blood
CC to Rhesus negative recipients in order to prevent sensitisation to the
CC Rhesus D antigen. The products can also be used as diagnostic reagents.

XX
SQ Sequence 125 AA;

Query Match 91.9%; Score 615; DB 19; Length 125;
Best Local Similarity 90.4%; Pred. No. 5,6e-50;
Matches 113; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 1 QVQLLESQGGVVPQGSILRVACVAGFTFRNFGMHWROAPGKGLRWVAFIWPDSANKGY 60
DB 1 QVQLLESQGGVVPQGSILRVACVAGFTFRNFGMHWROAPGKGLRWVAFIWPDSANKGY 60

QY 61 GDSVKGKFTVSRDNSKNTLYLQNNGLRAEDTAVYYCAREKAVRGISRYNYMDVWGKGT 120
DB 61 VDSVKGKFTVSRDNSKNTLYLQNNGLRAEDTAVYYCAREKALRGISRYNYLDVWGKGT 120

QY 121 VTIVSS 125
DB 121 VTIVSS 125

RESULT 6
AAW52226
ID AAW52226 standard; Protein; 125 AA.

XX AAW52226;
AC
XX
DT 12-JUN-1998 (first entry)
XX
DE Antibody LD2-5-VH chain sequence.

XX Antibody; variable heavy chain; VH chain; variable light chain; VL chain;
KW Rhesus D antigen; anti-Rhesus D immunoglobulin; HDN; therapy;
KM idiopathic thrombocytopenic purpura; haemolytic disease of the newborn.

XX
OS Homo sapiens.
XX
PN WO9749809-A1.
XX
PD 31-DEC-1997.
XX
PF 20-JUN-1997; 97WO-EP03253.
XX
PR 24-JUN-1996; 96EP-0810421.
XX
PA (ROTK-) ROTKREUZSTIFTUNG ZENT LAB BLUTSPENDE.
XX
PI Amstutz H, Imboden M, Miescher S, Morell A, Stadler B;
PI Vogel M;
XX
DR WPI; 1998-077173/07.
DR N-PSDB; AAV19750.
XX
XX New Rhesus D antigen binding polypeptide(s) - used to neutralise
PT Rhesus D antigen in therapy, e.g. for treating idiopathic
PT thrombocytopenic purpura
XX
PS Claim 1; Fig 8A; 68bp; English.

XX This sequence is the antibody LD2-5-VH chain sequence, which is a
CC polypeptide of the invention. The polypeptides are capable of forming
CC antigen binding structures with specificity for Rhesus D antigens which
CC include Rhesus D-specific CDR 1, CDR 2, and CDR 3 regions of pairs of
CC variable heavy (VH) and variable light (VL) chain sequences. The
CC antibodies are active against the Rhesus D antigen. They can be used for
CC treating disorders which would benefit from anti-Rhesus D immunoglobulin,
CC e.g. idiopathic thrombocytopenic purpura. They can also be used for the
CC protection of Rhesus negative women before or immediately after the birth
CC of a Rhesus positive child to prevent haemolytic disease of the newborn
CC (HDN) in subsequent pregnancies. In addition, anti-Rhesus D
CC immunoglobulin can be used after mistransfusions of Rhesus positive blood
CC to Rhesus negative recipients in order to prevent sensitisation to the
CC Rhesus D antigen. The products can also be used as diagnostic reagents.

XX
SQ Sequence 125 AA;

Query Match 91.9%; Score 615; DB 19; Length 125;
Best Local Similarity 89.6%; Pred. No. 5,6e-50;
Matches 112; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

QY 1 QVQLLESQGGVVPQGSILRVACVAGFTFRNFGMHWROAPGKGLRWVAFIWPDSANKGY 60
DB 1 QVQLLESQGGVVPQGSILRVACVAGFTFRNFGMHWROAPGKGLRWVAFIWPDSANKGY 60

QY 61 GDSVKGKFTVSRDNSKNTLYLQNNGLRAEDTAVYYCAREKAVRGISRYNYMDVWGKGT 120
DB 61 VDSVKGKFTVSRDNSKNTLYLQNNGLRAEDTAVYYCAREKALRGISRYNYLDVWGKGT 120

QY 121 VTIVSS 125
DB 121 VTIVSS 125

RESULT 7
AAW52222
ID AAW52222 standard; Protein; 125 AA.

XX AAW52222;
AC
XX
DT 12-JUN-1998 (first entry)
XX
DE Antibody LD2-1-VH chain sequence.

XX Antibody; variable heavy chain; VH chain; variable light chain; VL chain;
KW Rhesus D antigen; anti-Rhesus D immunoglobulin; HDN; therapy;
KM idiopathic thrombocytopenic purpura; haemolytic disease of the newborn.

XX
OS Homo sapiens.
XX
PN WO9749809-A1.
XX
PD 31-DEC-1997.
XX
PF 20-JUN-1997; 97WO-EP03253.
XX
PR 24-JUN-1996; 96EP-0810421.
XX
PA (ROTK-) ROTKREUZSTIFTUNG ZENT LAB BLUTSPENDE.
XX
PI Amstutz H, Imboden M, Miescher S, Morell A, Stadler B;
PI Vogel M;
XX
DR WPI; 1998-077173/07.
DR N-PSDB; AAV19746.
XX
XX New Rhesus D antigen binding polypeptide(s) - used to neutralise
PT Rhesus D antigen in therapy, e.g. for treating idiopathic
PT thrombocytopenic purpura
XX
PS Claim 1; Fig 6A; 68bp; English.

CC This sequence is the antibody LD2-1-VH chain sequence, which is a
CC polypeptide of the invention. The polypeptides are capable of forming
CC antigen binding structures with specificity for Rhesus D antigens which
CC include Rhesus D-specific CDR 1, CDR 2, and CDR 3 regions of pairs of
CC variable heavy (VH) and variable light (VL) chain sequences. The
CC antibodies are active against the Rhesus D antigen. They can be used for
CC treating disorders which would benefit from anti-Rhesus D immunoglobulin,
CC e.g. idiopathic thrombocytopenic purpura. They can also be used for the
CC protection of Rhesus negative women before or immediately after the birth
CC of a Rhesus positive child to prevent haemolytic disease of the newborn
CC (HDN) in subsequent pregnancies. In addition, anti-Rhesus D
CC immunoglobulin can be used after mistransfusions of Rhesus positive blood
CC to Rhesus negative recipients in order to prevent sensitisation to the
CC Rhesus D antigen. The products can also be used as diagnostic reagents.

SO Sequence 125 AA;

Query Match 91.3%; Score 611; DB 19; Length 125;
Best Local Similarity 88.8%; Pred. No. 1.3e-49;
Matches 111; Conservative 9; Mismatches 5; Indels 0; Gaps 0;

QY 1 QVTLSSGGGVVOPGSLRACVAGSFTFRNFGMHVWRQAPGKLEWVAFIWFDSNKG 60
DB 1 QVTLSSGGGVVOPGSLRACVAGSFTFRNFGMHVWRQAPGKLEWVAFIWFDSNKG 60
QY 61 GDSVKGKFTVSRDNRKNTLYLQNMGLRAEDTAVYYCAREKAVRGISRYNYMDVWGKGT 120
DB 61 VDSVKGKFTVSRDNRKNTLYLQNMGLRAEDTAVYYCAREKAVRGISRYNYMDVWGKGT 120
QY 121 VTIVSS 125
DB 121 VTIVSS 125

RESULT 8
AAW52228
ID AAW52228 standard; Protein; 126 AA.

AAW52228;

12-JUN-1998 (first entry)

Antibody LD2-10-VH chain sequence.

Antibody; variable heavy chain; VH chain; variable light chain; VL chain;
Rhesus D antigen; anti-Rhesus D immunoglobulin; HDN; therapy;

idiopathic thrombocytopenic purpura; haemolytic disease of the newborn.

Homo sapiens.

MO9749809-A1.

31-DEC-1997.

20-JUN-1997; 97WO-EP03253.

24-JUN-1996; 96EP-0810421.

(ROTK-) ROTKREUZSTIFTUNG ZENT LAB BLUTSPENDE.

Amstutz H, Imboden M, Miescher S, Morell A, Stadler B;
Vogel M;

WPI; 1998-077173/07.

N-PSDB; AAV19752.

New Rhesus D antigen binding poly:peptide(s) - used to neutralise
Rhesus D antigen in therapy, e.g. for treating idiopathic
thrombocytopenic purpura

Claim 1; Fig 9A; 68pp; English.

This sequence is the antibody LD2-10-VH chain sequence, which is a

CC polypeptide of the invention. The polypeptides are capable of forming
CC antigen binding structures with specificity for Rhesus D antigens which
CC include Rhesus D-specific CDR 1, CDR 2, and CDR 3 regions of pairs of
CC variable heavy (VH) and variable light (VL) chain sequences. The
CC antibodies are active against the Rhesus D antigen. They can be used for
CC treating disorders which would benefit from anti-Rhesus D immunoglobulin,
CC e.g. idiopathic thrombocytopenic purpura. They can also be used for the
CC protection of Rhesus negative women before or immediately after the birth
CC of a Rhesus positive child to prevent haemolytic disease of the newborn
CC (HDN) in subsequent pregnancies. In addition, anti-Rhesus D
CC immunoglobulin can be used after mistransfusions of Rhesus positive blood
CC to Rhesus negative recipients in order to prevent sensitisation to the
CC Rhesus D antigen. The products can also be used as diagnostic reagents.

SO Sequence 126 AA;

Query Match 89.8%; Score 600.5; DB 19; Length 126;
Best Local Similarity 88.1%; Pred. No. 1.3e-48;
Matches 111; Conservative 9; Mismatches 5; Indels 1; Gaps 1;

QY 1 QVTLSSGGGVVOPGSLRACVAGSFTFRNFGMHVWRQAPGKLEWVAFIWFDSNKG 60
DB 1 QVTLSSGGGVVOPGSLRACVAGSFTFRNFGMHVWRQAPGKLEWVAFIWFDSNKG 60
QY 61 GDSVKGKFTVSRDNRKNTLYLQNMGLRAEDTAVYYCAREKAVRGISRYNYMDVWGKGT 119
DB 61 VDSVKGKFTVSRDNRKNTLYLQNMGLRAEDTAVYYCAREKAVRGISRYNYMDVWGKGT 120
QY 120 TTVVSS 125
DB 121 TTVVSS 126

RESULT 9
AAW52218
ID AAW52218 standard; Protein; 125 AA.

AAW52218;

12-JUN-1998 (first entry)

Antibody LD1-110-VH chain sequence.

Antibody; variable heavy chain; VH chain; variable light chain; VL chain;
Rhesus D antigen; anti-Rhesus D immunoglobulin; HDN; therapy;

idiopathic thrombocytopenic purpura; haemolytic disease of the newborn.

Homo sapiens.

MO9749809-A1.

31-DEC-1997.

20-JUN-1997; 97WO-EP03253.

24-JUN-1996; 96EP-0810421.

(ROTK-) ROTKREUZSTIFTUNG ZENT LAB BLUTSPENDE.

Amstutz H, Imboden M, Miescher S, Morell A, Stadler B;
Vogel M;

WPI; 1998-077173/07.

N-PSDB; AAV19742.

New Rhesus D antigen binding poly:peptide(s) - used to neutralise
Rhesus D antigen in therapy, e.g. for treating idiopathic
thrombocytopenic purpura

Claim 1; Fig 4A; 68pp; English.

This sequence is the antibody LD1-110-VH chain sequence, which is a
polypeptide of the invention. The polypeptides are capable of forming

CC variable heavy (VH) and variable light (VL) chain sequences. The
 CC antibodies are active against the Rhesus D antigen. They can be used for
 CC treating disorders which would benefit from anti-Rhesus D immunoglobulin,
 CC e.g. idiopathic thrombocytopenic purpura. They can also be used for the
 CC protection of Rhesus negative women before or immediately after the birth
 CC of a Rhesus positive child to prevent haemolytic disease of the newborn
 CC (HDN). In subsequent pregnancies. In addition, anti-Rhesus D
 CC immunoglobulin can be used after mistransfusions of Rhesus positive blood
 CC to Rhesus negative recipients in order to prevent sensitisation to the
 CC Rhesus D antigen. The products can also be used as diagnostic reagents.

XX Sequence 125 AA;

Query Match 85.9%; Score 575; DB 19; Length 125;
 Best Local Similarity 84.7%; Pred. No. 3e-46;
 Matches 105; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

QY 1 QVTLSEGGGVVOPGSLRVACVAGSFTFRNPGMHWVROAPGKLEWVAFIFDASNKGY 60
 DB 1 QVTLSEGGGVVOPGSLRVACVAGSFTFRNPGMHWVROAPGKLEWVAFIFDASNKGY 60
 QY 61 GDSVKGFTVSRNDSKNTLYLQWNGLEAPDTAVYYCARERAVRGISRYNYMDVWGKGT 120
 DB 61 ADSVKGFTISRDNKNTLYLQWNGLEAPDTAVYYCARERAVRGISRYNYMDVWGKGT 120

QY 121 VTYS 124
 DB 121 VTYS 124

RESULT 12

AAW52230 standard; Protein; 125 AA.

XX AAW52230;

XX 12-JUN-1998 (first entry)

XX Antibody LD2-11-VH chain sequence.

XX Antibody; variable heavy chain; VH chain; variable light chain; VL chain;
 KW Rhesus D antigen; anti-Rhesus D immunoglobulin; HDN; therapy;
 XX idiopathic thrombocytopenic purpura; haemolytic disease of the newborn.

OS Homo sapiens.

PN MO9749809-A1.

PD 31-DEC-1997.

PF 20-JUN-1997; 97WO-EP03253.

PR 24-JUN-1996; 96EP-0810421.

PA (ROTK-) ROTKREUZSTIFTUNG ZENT LAB BLUTSPENDE.

PI Amstutz H, Imboden M, Miescher S, Morell A, Stadler B;

PI Vogel M;

DR MPI; 1998-077173/07.

DR N-PSDB; AAV19754.

PT New Rhesus D antigen binding poly:peptide(s) - used to neutralise

PT Rhesus D antigen in therapy, e.g. for treating idiopathic

XX thrombocytopenic purpura

XX Claim 1; Fig 10A; 68pp; English.

CC This sequence is the antibody LD2-11-VH chain sequence, which is a
 CC polypeptide of the invention. The polypeptides are capable of forming
 CC antigen binding structures with specificity for Rhesus D antigens which
 CC include Rhesus D-specific CDR 1, CDR 2, and CDR 3 regions of pairs of
 CC variable heavy (VH) and variable light (VL) chain sequences. The

CC antibodies are active against the Rhesus D antigen. They can be used for
 CC treating disorders which would benefit from anti-Rhesus D immunoglobulin,
 CC e.g. idiopathic thrombocytopenic purpura. They can also be used for the
 CC protection of Rhesus negative women before or immediately after the birth
 CC of a Rhesus positive child to prevent haemolytic disease of the newborn
 CC (HDN). In subsequent pregnancies. In addition, anti-Rhesus D
 CC immunoglobulin can be used after mistransfusions of Rhesus positive blood
 CC to Rhesus negative recipients in order to prevent sensitisation to the
 CC Rhesus D antigen. The products can also be used as diagnostic reagents.

XX Sequence 125 AA;

Query Match 85.1%; Score 569; DB 19; Length 125;
 Best Local Similarity 84.0%; Pred. No. 1.1e-45;
 Matches 105; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

QY 1 QVTLSEGGGVVOPGSLRVACVAGSFTFRNPGMHWVROAPGKLEWVAFIFDASNKGY 60
 DB 1 QVTLSEGGGVVOPGSLRVACVAGSFTFRNPGMHWVROAPGKLEWVAFIFDASNKGY 60
 QY 61 GDSVKGFTVSRNDSKNTLYLQWNGLEAPDTAVYYCARERAVRGISRYNYMDVWGKGT 120
 DB 61 ADSVKGFTISRDNKNTLYLQWNGLEAPDTAVYYCARERAVRGISRYNYMDVWGKGT 120

QY 121 VTYS 125
 DB 121 VTYS 125

RESULT 13

AAW52224 standard; Protein; 125 AA.

XX AAW52224;

XX 12-JUN-1998 (first entry)

XX Antibody LD2-4-VH chain sequence.

XX Antibody; variable heavy chain; VH chain; variable light chain; VL chain;
 KW Rhesus D antigen; anti-Rhesus D immunoglobulin; HDN; therapy;
 XX idiopathic thrombocytopenic purpura; haemolytic disease of the newborn.

OS Homo sapiens.

PN MO9749809-A1.

PD 31-DEC-1997.

PF 20-JUN-1997; 97WO-EP03253.

PR 24-JUN-1996; 96EP-0810421.

PA (ROTK-) ROTKREUZSTIFTUNG ZENT LAB BLUTSPENDE.

PI Amstutz H, Imboden M, Miescher S, Morell A, Stadler B;

PI Vogel M;

DR MPI; 1998-077173/07.

DR N-PSDB; AAV19748.

PT New Rhesus D antigen binding poly:peptide(s) - used to neutralise

PT Rhesus D antigen in therapy, e.g. for treating idiopathic

XX thrombocytopenic purpura

XX Claim 1; Fig 7A; 68pp; English.

CC This sequence is the antibody LD2-4-VH chain sequence, which is a
 CC polypeptide of the invention. The polypeptides are capable of forming
 CC antigen binding structures with specificity for Rhesus D antigens which
 CC include Rhesus D-specific CDR 1, CDR 2, and CDR 3 regions of pairs of
 CC variable heavy (VH) and variable light (VL) chain sequences. The
 CC antibodies are active against the Rhesus D antigen. They can be used for

CC treating disorders which would benefit from anti-Rhesus D immunoglobulin,
 CC e.g. idiopathic thrombocytopenic purpura. They can also be used for the
 CC protection of Rhesus negative women before or immediately after the birth
 CC of a Rhesus positive child to prevent haemolytic disease of the newborn
 CC (HDN) in subsequent pregnancies. In addition, anti-Rhesus D
 CC immunoglobulin can be used after mistransfusions of Rhesus positive blood
 CC to Rhesus negative recipients in order to prevent sensitisation to the
 CC Rhesus D antigen. The products can also be used as diagnostic reagents.

XX Sequence 125 AA;

Query Match 85.1%; Score 569; DB 19; Length 125;

Best Local Similarity 84.0%; Pred. No. 1.1e-45; Matches 105; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

QY 1 QVTLSEGGGVVPGGSLRVAACVAGSFTFRNFGMHWRQAPGKGLBVAFTWPDASNKGY 60
 DB 1 QVTLSEGGGVVPGGSLRVAACVAGSFTFRNFGMHWRQAPGKGLBVAFTWPDASNKGY 60
 QY 61 GDSVKGKFTVSRDSSKNTLYLQNMGLRAEDTAVYYCAREKAVRGISRYNYMDVWGKGT 120
 DB 61 AESVKGKFTISRDTSKNTLYLQNMGLRAEDTAVYYCAREKAVRGISRYNYMDVWGKGT 120

QY 121 VTVSS 125
 DB 121 VTVSS 125

RESULT 14

AAW52216 ID AAW52216 standard; Protein; 125 AA.

AC AAW52216;

DT 12-JUN-1998 (first entry)

DE Antibody LD1-84-VH chain sequence.

XX Antibody; variable heavy chain; VH chain; variable light chain; VL chain;
 KW Rhesus D antigen; anti-Rhesus D immunoglobulin; HDN; therapy;
 KM idiopathic thrombocytopenic purpura; haemolytic disease of the newborn.

XX Homo sapiens.

XX MO9749809-A1.

XX 31-DEC-1997.

XX 20-JUN-1997; 97WO-EP03253.

XX 24-JUN-1996; 96EP-0810421.

XX (ROTK-) ROTKREUZSTIFTUNG ZENT LAB BLUTSPENDE.

XX Amstutz H, Imboden M, Miescher S, Morell A, Stadler B;
 PI Vogel M;

XX WPI; 1998-077173/07.

XX N-PSDB; AAV19740.

PT New Rhesus D antigen binding polypeptide(s) - used to neutralise
 PT Rhesus D antigen in therapy, e.g. for treating idiopathic
 PT thrombocytopenic purpura

PS Claim 1; Fig 3A; 68pp; English.

XX This sequence is the antibody LD1-84-VH chain sequence, which is a
 CC polypeptide of the invention. The polypeptides are capable of forming
 CC antigen binding structures with specificity for Rhesus D antigens which
 CC include Rhesus D-specific CDR 1, CDR 2, and CDR 3 regions of pairs of
 CC variable heavy (VH) and variable light (VL) chain sequences. The
 CC antibodies are active against the Rhesus D antigen. They can be used for
 CC treating disorders which would benefit from anti-Rhesus D immunoglobulin,

CC e.g. idiopathic thrombocytopenic purpura. They can also be used for the
 CC protection of Rhesus negative women before or immediately after the birth
 CC of a Rhesus positive child to prevent haemolytic disease of the newborn
 CC (HDN) in subsequent pregnancies. In addition, anti-Rhesus D
 CC immunoglobulin can be used after mistransfusions of Rhesus positive blood
 CC to Rhesus negative recipients in order to prevent sensitisation to the
 CC Rhesus D antigen. The products can also be used as diagnostic reagents.

XX Sequence 125 AA;

Query Match 85.1%; Score 569; DB 19; Length 125;

Best Local Similarity 84.0%; Pred. No. 1.1e-45; Matches 105; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

QY 1 QVTLSEGGGVVPGGSLRVAACVAGSFTFRNFGMHWRQAPGKGLBVAFTWPDASNKGY 60
 DB 1 QVTLSEGGGVVPGGSLRVAACVAGSFTFRNFGMHWRQAPGKGLBVAFTWPDASNKGY 60
 QY 61 GDSVKGKFTVSRDSSKNTLYLQNMGLRAEDTAVYYCAREKAVRGISRYNYMDVWGKGT 120
 DB 61 AESVKGKFTISRDTSKNTLYLQNMGLRAEDTAVYYCAREKAVRGISRYNYMDVWGKGT 120

QY 121 VTVSS 125
 DB 121 VTVSS 125

RESULT 15

AAW52214 ID AAW52214 standard; Protein; 125 AA.

AC AAW52214;

DT 12-JUN-1998 (first entry)

DE Antibody LD1-52-VH chain sequence.

XX Antibody; variable heavy chain; VH chain; variable light chain; VL chain;
 KW Rhesus D antigen; anti-Rhesus D immunoglobulin; HDN; therapy;
 KM idiopathic thrombocytopenic purpura; haemolytic disease of the newborn.

XX Homo sapiens.

XX MO9749809-A1.

XX 31-DEC-1997.

XX 20-JUN-1997; 97WO-EP03253.

XX 24-JUN-1996; 96EP-0810421.

XX (ROTK-) ROTKREUZSTIFTUNG ZENT LAB BLUTSPENDE.

XX Amstutz H, Imboden M, Miescher S, Morell A, Stadler B;
 PI Vogel M;

XX WPI; 1998-077173/07.

XX N-PSDB; AAV19738.

PT New Rhesus D antigen binding polypeptide(s) - used to neutralise
 PT Rhesus D antigen in therapy, e.g. for treating idiopathic
 PT thrombocytopenic purpura

PS Claim 1; Fig 2A; 68pp; English.

XX This sequence is the antibody LD1-52-VH chain sequence, which is a
 CC polypeptide of the invention. The polypeptides are capable of forming
 CC antigen binding structures with specificity for Rhesus D antigens which
 CC include Rhesus D-specific CDR 1, CDR 2, and CDR 3 regions of pairs of
 CC variable heavy (VH) and variable light (VL) chain sequences. The
 CC antibodies are active against the Rhesus D antigen. They can be used for
 CC treating disorders which would benefit from anti-Rhesus D immunoglobulin,
 CC e.g. idiopathic thrombocytopenic purpura. They can also be used for the

CC protection of Rhesus negative women before or immediately after the birth
CC of a Rhesus positive child to prevent haemolytic disease of the newborn
CC (HDN) in subsequent pregnancies. In addition, anti-Rhesus D
CC immunoglobulin can be used after mistransfusions of Rhesus positive blood
CC to Rhesus negative recipients in order to prevent sensitisation to the
CC Rhesus D antigen. The products can also be used as diagnostic reagents.
XX

SQ Sequence 125 AA;

Query Match 84.3%; Score 564; DB 19; Length 125;
Best Local Similarity 83.2%; Pred. No. 3.2e-45;

Matches 104; Conservative 8; Mismatches 13; Indels 0; Gaps 0;

| | | | |
|----|-----|---|-----|
| QY | 1 | QVRLSSGGGVOPGSGIRVACVAGFTFRNFGMHWVROAPGKGLKLVAFIFPDASNKGY | 60 |
| DB | 1 | QVRLSSGGGVOPGSGIRLSCASGPAIRSSGMHWVROAPGKGLKLVAFIFPDGSIKSY | 60 |
| QY | 61 | GDSVKGKRFIVSRDNSKNTLYLQWNGLRADPTAVYYCAREKAVRGISRYNYMDVWGKGT | 120 |
| DB | 61 | AESVKGKRFITSRDTSKNTLYLQWRSLSADDTAVYYCARDKAVRGISRYNYMDVWGKGT | 120 |
| QY | 121 | VTVSS | 125 |
| DB | 121 | VTVSS | 125 |

Search completed: January 22, 2004, 11:51:20
Job time : 40.1304 secs


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; SOFTWARE:PatentIn Ver. 2.0
; SEQ ID NO 22
; LENGTH: 125
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain D17
US-09-848-798-22

Query Match
Best Local Similarity 81.2%; Score 543; DB 11; Length 125;
Matches 100; Conservative 9; Mismatches 16; Indels 0; Gaps 0

QY 1 QVKLLSEGGGVQPGGSLRVACVAGFTFRNGMHWRAQAPKGLIEWAFIFPDASNKY 60
   ::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 1 EVQLLESGGGVQPGPSRLRLSCVSGFTFNNGMHWRAQAPKGLIEWAIVFDGSNKYY 60

QY 61 GDSVYGRFTVSRDNSKNTLYLQMGRLRAEDTAVVYCARAKGISRNVYMDVWGKGT 120
   |||||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 61 ADSVYGRFTISRDNKNTLYLQMGSLRAEDTAVVYCAARENQIKLSRIYLYDYGCGTL 120

QY 121 TVTSS 125
   |||||
Db 121 TVTSS 125

RESULT 6
US-09-848-798-17
; Sequence 17, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: R1(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/848,798
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 126
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain D12
US-09-848-798-17

Query Match
Best Local Similarity 81.1%; Score 542.5; DB 11; Length 126;
Matches 101; Conservative 12; Mismatches 12; Indels 1; Gaps 1

QY 1 QVKLLSEGGGVQPGGSLRVACVAGFTFRNGMHWRAQAPKGLIEWAFIFPDASNKY 60
   ::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 1 EVQLLESGGGVQPGPSRLRLCAAGSGFSPRSYGMHWRAQAPRGLEWVAFITFDGSNKYY 60

QY 61 GDSVYGRFTVSRDNSKNTLYLQMGRLRAEDTAVVYCARAKA-VRGISRNVYMDVWGKGT 119
   |||||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 61 VDSVYGRFTISRDNKNTLYLEMNSLRVDDTAVVYCARBASMLRGISRYYAMDVWGPGT 120

QY 120 TVTSS 125
   |||||
Db 121 TVTSS 126

RESULT 7
US-09-848-798-14
; Sequence 14, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:

```

```

APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
FILE REFERENCE: 09596-4202
CURRENT APPLICATION NUMBER: US/09/848,798
PRIOR FILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 14
LENGTH: 126
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: anti-Rh(D) chain D10
US-09-848-798-15

Query Match      80.9%; Score 541.5; DB 11; Length 126;
Best Local Similarity 81.7%; Pred. No. 2.6e-43;
Matches 103; Conservative 9; Mismatches 13; Indels 1; Gaps 1

1 QVXLLSEGGGVQVGGSLRVAQVSGFFRRFGMGHWVQAPQKGLIEWAFIFDASNKGY 60
  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1 EVQLLESGGGVQVQGRSIRLSCASKFTLYNYGMHWVQAPQKGLIEWAFIFDGSNKYY 60
  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

61 GDSVYKGRFTVSRRDSKNTLYLQNMGLRAEDTAVVYCAEAKVR-GISRNYNYMDWGKGT 119
  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
61 EDVSKGRFTVSRRDSKNTLYLQNMGLRAEDTAVVYCAEAGSKVALSRYYNYMDWGQGT 120
  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Db
120 TTVTVSS 125
  |||||
121 TTVTVSS 126

RESULT 8
US-09-848-798-15
; Sequence 15, Application US/09848798
; Publication No. US20030040605a1
GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
FILE REFERENCE: 09596-4202
CURRENT APPLICATION NUMBER: US/09/848,798
CURRENT FILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 15
LENGTH: 126
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: anti-Rh(D) chain D10
US-09-848-798-15

Query Match      80.9%; Score 541.5; DB 11; Length 126;
Best Local Similarity 81.7%; Pred. No. 2.6e-43;
Matches 103; Conservative 9; Mismatches 13; Indels 1; Gaps 1

1 QVXLLSEGGGVQVGGSLRVAQVSGFFRRFGMGHWVQAPQKGLIEWAFIFDASNKGY 60
  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1 EVQLLESGGGVQVQGRSIRLSCASKFTLYNYGMHWVQAPQKGLIEWAFIFDGSNKYY 60
  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

61 GDSVYKGRFTVSRRDSKNTLYLQNMGLRAEDTAVVYCAEAKVR-GISRNYNYMDWGKGT 119
  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
61 EDVSKGRFTVSRRDSKNTLYLQNMGLRAEDTAVVYCAEAGSKVALSRYYNYMDWGQGT 120
  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Db
120 TTVTVSS 125
  |||||
121 TTVTVSS 126

```

Qy 120 TTTVSS 125
121 TTTVSS 126

RESULT 9
US-09-848-798-147

Sequence 147, Application US/09848798
Publication No. US20030040605A1

GENERAL INFORMATION:

APPLICANT: Siegel, Donald L.

TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL

FILE REFERENCE: 09596-4202

CURRENT APPLICATION NUMBER: US/09/848,798

PRIOR FILING DATE: 2001-05-04

PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29

PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11

NUMBER OF SEQ ID NOS: 224

SOFTWARE: Patentln Ver. 2.0

SEQ ID NO 147

LENGTH: 126

TYPE: PR1

ORGANISM: Homo sapiens

FEATURE:

OTHER INFORMATION: anti-Rh(D) antibody clone SH32

US-09-848-798-147

Query Match 80.9%; Score 541.5; DB 11; Length 126;
Best Local Similarity 81.7%; Pred. No. 2.6e-43;
Matches 103; Conservative 9; Mismatches 13; Indels 1; Gaps 1;

Qy 1 QVTLSEGGGVOPGSLRVACVAGSFTFRNFGMHWRQAPGKLEWAFIWDASNGY 60

1 EVQLLESGGGVOPGSLRVACVAGSFTFRNFGMHWRQAPGKLEWAFIWDASNGY 60

Db 61 GDSVKGKFTVSRNSKNTLYLQNMGLRAEDTAVYYCAREKAVR-GISRYNYNDVWGKGT 119

61 EDSVKGKFTVSRNSKNTLYLQNMGLRAEDTAVYYCAREKAVR-GISRYNYNDVWGKGT 120

Qy 120 TTTVSS 125

121 TTTVSS 126

RESULT 10
US-09-848-798-148

Sequence 148, Application US/09848798
Publication No. US20030040605A1

GENERAL INFORMATION:

APPLICANT: Siegel, Donald L.

TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL

FILE REFERENCE: 09596-4202

CURRENT APPLICATION NUMBER: US/09/848,798

PRIOR FILING DATE: 2001-05-04

PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29

PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11

NUMBER OF SEQ ID NOS: 224

SOFTWARE: Patentln Ver. 2.0

SEQ ID NO 148

LENGTH: 126

TYPE: PR1

ORGANISM: Homo sapiens

FEATURE:

OTHER INFORMATION: anti-Rh(D) antibody clone SH37

US-09-848-798-148

Query Match 80.9%; Score 541.5; DB 11; Length 126;
Best Local Similarity 81.7%; Pred. No. 2.6e-43;
Matches 103; Conservative 9; Mismatches 13; Indels 1; Gaps 1;

Qy 1 QVTLSEGGGVOPGSLRVACVAGSFTFRNFGMHWRQAPGKLEWAFIWDASNGY 60

1 EVQLLESGGGVOPGSLRVACVAGSFTFRNFGMHWRQAPGKLEWAFIWDASNGY 60

Db 61 GDSVKGKFTVSRNSKNTLYLQNMGLRAEDTAVYYCAREKAVR-GISRYNYNDVWGKGT 119

61 EDSVKGKFTVSRNSKNTLYLQNMGLRAEDTAVYYCAREKAVR-GISRYNYNDVWGKGT 120

Qy 120 TTTVSS 125

121 TTTVSS 126

RESULT 11
US-09-848-798-16

Sequence 16, Application US/09848798
Publication No. US20030040605A1

GENERAL INFORMATION:

APPLICANT: Siegel, Donald L.

TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL

FILE REFERENCE: 09596-4202

CURRENT APPLICATION NUMBER: US/09/848,798

PRIOR FILING DATE: 2001-05-04

PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29

PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11

NUMBER OF SEQ ID NOS: 224

SOFTWARE: Patentln Ver. 2.0

SEQ ID NO 16

LENGTH: 126

TYPE: PR1

ORGANISM: Homo sapiens

FEATURE:

OTHER INFORMATION: anti-Rh(D) chain D11

US-09-848-798-16

Query Match 80.6%; Score 539.5; DB 11; Length 126;
Best Local Similarity 81.0%; Pred. No. 4e-43;
Matches 102; Conservative 10; Mismatches 13; Indels 1; Gaps 1;

Qy 1 QVTLSEGGGVOPGSLRVACVAGSFTFRNFGMHWRQAPGKLEWAFIWDASNGY 60

1 EVQLLESGGGVOPGSLRVACVAGSFTFRNFGMHWRQAPGKLEWAFIWDASNGY 60

Db 61 GDSVKGKFTVSRNSKNTLYLQNMGLRAEDTAVYYCAREKAVR-GISRYNYNDVWGKGT 119

61 EDSVKGKFTVSRNSKNTLYLQNMGLRAEDTAVYYCAREKAVR-GISRYNYNDVWGKGT 120

Qy 120 TTTVSS 125

121 TTTVSS 126

RESULT 12
US-09-848-798-23

Sequence 23, Application US/09848798
Publication No. US20030040605A1

GENERAL INFORMATION:

APPLICANT: Siegel, Donald L.

TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL

FILE REFERENCE: 09596-4202

CURRENT APPLICATION NUMBER: US/09/848,798

PRIOR FILING DATE: 2001-05-04

PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29

PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11

NUMBER OF SEQ ID NOS: 224

SOFTWARE: Patentln Ver. 2.0

SEQ ID NO 23

LENGTH: 126

TYPE: PR1

ORGANISM: Homo sapiens

FEATURE:

OTHER INFORMATION: anti-Rh(D) antibody clone SH37

US-09-848-798-23

;; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
;; NUMBER OF SEQ ID NOS: 224
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO: 23
;; LENGTH: 125
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; OTHER INFORMATION: anti-Rh(D) chain D18
US-09-848-798-23

Query Match
Best Local Similarity 80.0%; Score 535; DB 11; Length 125;
Matches 99; Conservative 9; Mismatches 17; Indels 0; Gaps 0;

QY 1 QVLLBSGGGVVOPGSLRVACVAGSFTFRNFGMHVROAPGKLEWVAFIWFDASNKGY 60
DB 1 EVQLLESGGGVVOPGSLRLSCAASGFTFSRNGMHVROAPGKLEWVAFIWFDGSKNXY 60
61 GDSVKGKFTVSRDNRKNTLYLQWNGLRADPTAVYYCAREKAVRGISRYNYMDWGKGT 120
DB 61 ADSVKGKFTISRDNKNTLYLQWNSLRADPTAVYYCAREKQIKLSKRYLYFPDYGQGT 120

QY 121 TVTVSS 125
DB 121 TVTVSS 125

RESULT 13
US-09-848-798-139
;; Sequence 139, Application US/09848798
;; Publication No. US20030040605A1
;; GENERAL INFORMATION:
;; APPLICANT: Siegel, Donald L.
;; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
;; FILE REFERENCE: 09596-42U2
;; CURRENT APPLICATION NUMBER: US/09/848,798
;; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
;; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
;; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
;; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
;; NUMBER OF SEQ ID NOS: 224
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO: 139
;; LENGTH: 127
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; OTHER INFORMATION: anti-Rh(D) antibody clone SH10
US-09-848-798-139

Query Match
Best Local Similarity 79.7%; Score 533; DB 11; Length 127;
Matches 101; Conservative 14; Mismatches 10; Indels 2; Gaps 2;

QY 1 QVLL-BSGGGVVOPGSLRVACVAGSFTFRNFGMHVROAPGKLEWVAFIWFDASNK 59
DB 1 EVQLLESGGGVVOPGSLRLSCAASGFTFSRNGMHVROAPGKLEWVAFIWFDGSKN 60
60 YGDSVKGKFTVSRDNRKNTLYLQWNGLRADPTAVYYCAREKAV-RGISRYNYMDWGK 118
DB 61 YADSVKGKFTISRDNKNTLYLQWNSLRADPTAVYYCAREKALRGLTRMSYGDWVG 120

QY 119 TVTVSS 125
DB 121 TVTVSS 127

RESULT 14
US-09-848-798-145
;; Sequence 145, Application US/09848798

;; Publication No. US20030040605A1
;; GENERAL INFORMATION:
;; APPLICANT: Siegel, Donald L.
;; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
;; FILE REFERENCE: 09596-42U2
;; CURRENT APPLICATION NUMBER: US/09/848,798
;; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
;; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
;; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
;; NUMBER OF SEQ ID NOS: 224
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO: 145
;; LENGTH: 127
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; OTHER INFORMATION: anti-Rh(D) antibody clone SH25
US-09-848-798-145

Query Match
Best Local Similarity 79.2%; Score 530; DB 11; Length 127;
Matches 101; Conservative 11; Mismatches 13; Indels 2; Gaps 2;

QY 1 QVLL-BSGGGVVOPGSLRVACVAGSFTFRNFGMHVROAPGKLEWVAFIWFDASNK 59
DB 1 EVQLLESGGGVVOPGSLRLSCAASGFTFSRNGMHVROAPGKLEWVAFIWFDGSKN 60
60 YGDSVKGKFTVSRDNRKNTLYLQWNGLRADPTAVYYCARE-KAVRISRYNYMDWGK 118
DB 61 YDSVKGKFTISRDNKNTLYLQWNSLRADPTAVYYCAREKAPLRGISRYNYMDWVG 120

QY 119 TVTVSS 125
DB 121 TVTVSS 127

RESULT 15
US-09-848-798-9
;; Sequence 9, Application US/09848798
;; Publication No. US20030040605A1
;; GENERAL INFORMATION:
;; APPLICANT: Siegel, Donald L.
;; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
;; FILE REFERENCE: 09596-42U2
;; CURRENT APPLICATION NUMBER: US/09/848,798
;; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
;; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
;; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
;; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
;; NUMBER OF SEQ ID NOS: 224
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO: 9
;; LENGTH: 125
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; OTHER INFORMATION: anti-Rh(D) chain D03
US-09-848-798-9

Query Match
Best Local Similarity 78.9%; Score 528; DB 11; Length 125;
Matches 98; Conservative 10; Mismatches 17; Indels 0; Gaps 0;

QY 1 QVLLBSGGGVVOPGSLRVACVAGSFTFRNFGMHVROAPGKLEWVAFIWFDASNK 60
DB 1 EVQLLESGGGVVOPGSLRLSCAASGFTFSRNGMHVROAPGKLEWVAFIWFDGSKN 60
61 GDSVKGKFTVSRDNRKNTLYLQWNGLRADPTAVYYCAREKAVRGISRYNYMDWGKGT 120

Db 61 AD5VKGRFTVSRDNRKNTLYLQWNSLRAPDTAVVYCCAREEVVRGVILMSRKFDTMCGQTL 120

Qy 121 VTVSS 125

Db 121 VTVSS 125

Search completed: January 22, 2004, 12:00:41
Job time : 38.5 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 22, 2004, 11:44:30 ; Search time 14.1522 Seconds
(without alignments)
713.510 Million cell updates/sec

Title: US-09-147-443D-60

Sequence: 1 VMTQSPSSLSASVGRVTIT.....CQGSYTPYTFGQGTKLKIK 105

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|---------------------------|
| 1 | 487 | 89.7 | 109 | 2 | S31981 Ig kappa chain - h |
| 2 | 486 | 89.5 | 127 | 2 | S40367 Ig kappa chain V-J |
| 3 | 483 | 89.0 | 109 | 2 | S31998 Ig kappa chain - h |
| 4 | 482 | 88.8 | 123 | 2 | S40331 Ig kappa chain - h |
| 5 | 476 | 87.7 | 108 | 2 | B49047 Ig kappa chain V r |
| 6 | 474 | 87.3 | 109 | 2 | S31978 Ig kappa chain - h |
| 7 | 472 | 86.9 | 108 | 2 | S47182 Ig kappa chain - h |
| 8 | 465 | 85.6 | 108 | 2 | S44122 Ig kappa chain V r |
| 9 | 461 | 84.9 | 109 | 2 | S31979 Ig kappa chain - h |
| 10 | 460 | 84.7 | 108 | 2 | S31977 Ig kappa chain - h |
| 11 | 459 | 84.5 | 129 | 2 | S52793 Ig kappa chain V r |
| 12 | 458 | 84.3 | 129 | 1 | K1HUMK Ig kappa chain pre |
| 13 | 457 | 84.2 | 108 | 1 | K1HUMD Ig kappa chain V-I |
| 14 | 457 | 84.2 | 109 | 2 | S31980 Ig kappa chain - h |
| 15 | 456 | 84.0 | 108 | 2 | S19674 Ig kappa chain V r |
| 16 | 456 | 83.6 | 129 | 2 | S40317 Ig kappa chain - h |
| 17 | 454 | 83.6 | 122 | 2 | S40314 Ig kappa chain - h |
| 18 | 452 | 83.2 | 107 | 2 | K16264 Ig lambda chain V |
| 19 | 452 | 83.2 | 108 | 1 | K1HUMU Ig kappa chain V-I |
| 20 | 452 | 83.2 | 122 | 2 | S40370 Ig kappa chain - h |
| 21 | 448 | 82.7 | 129 | 2 | S52792 Ig kappa chain V r |
| 22 | 448 | 82.5 | 109 | 2 | S32001 Ig kappa chain - h |
| 23 | 447 | 82.5 | 120 | 2 | S46370 Ig kappa chain V-J |
| 24 | 447 | 82.3 | 108 | 2 | K1HURE Ig kappa chain V-I |
| 25 | 445 | 82.0 | 109 | 2 | S31983 Ig kappa chain - h |
| 26 | 442 | 81.4 | 109 | 2 | UN0286 Ig kappa chain V-J |
| 27 | 440 | 81.0 | 117 | 2 | S46371 Ig kappa chain V-J |
| 28 | 438.5 | 80.8 | 125 | 2 | S40315 Ig kappa chain - h |
| 29 | 437.5 | 80.6 | 107 | 2 | S36275 Ig lambda chain V |

| | | | | | |
|----|-------|------|-----|---|---------------------------|
| 30 | 437 | 80.5 | 125 | 2 | S40333 Ig kappa chain V-J |
| 31 | 435 | 80.1 | 129 | 2 | S40369 Ig kappa chain - h |
| 32 | 434 | 79.9 | 108 | 1 | K1HOUU Ig kappa chain V-I |
| 33 | 434 | 79.9 | 117 | 2 | S24206 Ig kappa chain V r |
| 34 | 433 | 79.7 | 125 | 2 | S40350 Ig kappa chain - h |
| 35 | 433 | 79.7 | 128 | 2 | S46372 Ig kappa chain var |
| 36 | 432 | 79.6 | 126 | 2 | S40335 Ig kappa chain V-J |
| 37 | 432 | 79.6 | 129 | 2 | S52789 Ig kappa chain V r |
| 38 | 431 | 79.4 | 107 | 2 | JL0139 Ig kappa chain V r |
| 39 | 431 | 79.4 | 108 | 1 | K1HUBN Ig kappa chain V-I |
| 40 | 430.5 | 79.3 | 106 | 2 | PC2397 anti-tetanus toxin |
| 41 | 430.5 | 79.3 | 109 | 1 | K1HUMV Ig kappa chain V-I |
| 42 | 430 | 79.2 | 107 | 2 | S36262 Ig lambda chain V |
| 43 | 430 | 79.2 | 125 | 2 | S40349 Ig kappa chain V-J |
| 44 | 429 | 79.0 | 107 | 2 | S36269 Ig lambda chain V |
| 45 | 428 | 78.8 | 132 | 2 | S38646 Ig kappa chain V r |

ALIGNMENTS

RESULT 1

S31981
Ig kappa chain - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C/Accession: S31981
R/Portolano, S.; Chazenbalk, G.D.; Hutchison, S.J.; McLachlan, S.M.; Rapoport, B.
Submitted to the EMBL Data Library, June 1992
A/Description: Lack of promiscuity in autoantigen-specific H and L chain combinations as
A/Reference number: S31977
A/Accession: S31981
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-109 <FOR>
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotrimer; immunoglobulin
F/16-90/Domain: immunoglobulin homology <IMM>

Query Match 89.7%; Score 487; DB 2; Length 109;
Best Local Similarity 88.6%; Pred. No. 2.6e-36;
Matches 93; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 1 VMTQSPSSLSASVGRVTITCRASQSIIRYIMWYOHKPKAPKLTHTASSLSQSGVPSRF 60
|||||
DB 3 VMTQSPSSLSASVGRVTITCRASQDISRYLMWYQKPKAPKLTHTASTLESVPSGR 62
QY 61 SGSGSGTDFLTITSSLPEDPATYVYCQGSYTPYTFGQGTKLKIK 105
|||||
DB 63 SGSGSGTDFLTITSSLPEDPATYVYCQGSYTPYTFGQGTKLEIK 107

RESULT 2

S40367
Ig kappa chain V-J-C region - human
C/Species: Homo sapiens (man)
C/Date: 15-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C/Accession: S40367
R/Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A/Title: Expressed human immunoglobulin chi genes and their hypermutation.
A/Reference number: S40312; PMID:94080891; PMID:8258341
A/Accession: S40367
A/Status: preliminary; translation not shown
A/Molecule type: mRNA
A/Residues: 1-127 <ILV>
A/Cross-references: EMBL:X72477
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotrimer; immunoglobulin
F/33-107/Domain: immunoglobulin homology <IMM>

Query Match 89.5%; Score 486; DB 2; Length 127;

Best Local Similarity 90.4%; Pred. No. 3.7e-36;
Matches 94; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 2 MTQSPSSLSASVGDRTVITTCRASQSIIRYLNWYQHKRGKAPKLLIHFTASSLSQGVPSRFS 61
DB 21 MTQSPSSLSASVGDRTVITTCRASQSIIRYLNWYQHKRGKAPKLLIHFTASSLSQGVPSRFS 80
QY 62 GSVSGTDFLTITSLQPEDFATYCCOQSYTTPYTFGGTKLQIK 105
DB 81 GSVSGTDFLTITSLQPEDFATYCCOQSYTTPYTFGGTKLQIK 124

RESULT 3

S31998
Ig kappa chain - human (fragment)

C/Species: Homo sapiens (man)
C/Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000
C/Accession: S31998
R/Portolano, S.; Chazenbalk, G.D.; Hutchison, S.J.; McLachlan, S.M.; Rapoport, B.
Submitted to the EMBL Data Library, June 1992
A/Description: Lack of promiscuity in autoantigen-specific H and L chain combinations as
A/Reference number: S31977
A/Accession: S31998
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-109 <PDR>
A/Cross-references: EMBL:Z15081, NID:G38501, PIRN:CA178790.1, PID:G38502
C/Superfamily: Immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/16-90/Domain: immunoglobulin homology <IMM>

Query Match 89.0%; Score 483; DB 2; Length 109;
Best Local Similarity 89.5%; Pred. No. 5.8e-36;
Matches 94; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 VMTQSPSSLSASVGDRTVITTCRASQSIIRYLNWYQHKRGKAPKLLIHFTASSLSQGVPSRFS 60
DB 3 VMTQSPSSLSASVGDRTVITTCRASQSIIRYLNWYQHKRGKAPKLLIHFTASSLSQGVPSRFS 62
QY 61 GSVSGTDFLTITSLQPEDFATYCCOQSYTTPYTFGGTKLQIK 105
DB 63 GSVSGTDFLTITSLQPEDFATYCCOQSYTTPYTFGGTKLQIK 107

RESULT 4

S40331

Ig kappa chain - human

C/Species: Homo sapiens (man)
C/Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C/Accession: S40331
R/Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A/Title: Expressed human immunoglobulin chi genes and their hypermutation.
A/Reference number: S40332; MUID:94080891; PMID:8258341
A/Accession: S40331
A/Status: preliminary; translation not shown
A/Molecule type: mRNA
A/Residues: 1-123 <KBA>
A/Cross-references: EMBL:X72441, NID:G44350, PIRN:CA51109.1, PID:G44351
C/Superfamily: Immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/32-106/Domain: immunoglobulin homology <IMM>

Query Match 88.8%; Score 482; DB 2; Length 123;
Best Local Similarity 90.4%; Pred. No. 8.1e-36;
Matches 94; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 2 MTQSPSSLSASVGDRTVITTCRASQSIIRYLNWYQHKRGKAPKLLIHFTASSLSQGVPSRFS 61
DB 20 MTQSPSSLSASVGDRTVITTCRASQSIIRYLNWYQHKRGKAPKLLIHFTASSLSQGVPSRFS 79
QY 62 GSVSGTDFLTITSLQPEDFATYCCOQSYTTPYTFGGTKLQIK 105

DB 80 GSVSGTDFLTITSLQPEDFATYCCOQSYTTPYTFGGTKLQIK 123

RESULT 5

B49047

Ig kappa chain V region (monoclonal strictional autoantibody StrAB SA-1A) - human (fragme

C/Species: Homo sapiens (man)
C/Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C/Accession: B49047
R/Victor, K.D.; Pascual, V.; Williams, C.L.; Lennon, V.A.; Capra, J.D.
Eur. J. Immunol. 22, 2231-2236, 1992
A/Title: Human monoclonal strictional autoantibodies isolated from thymic B lymphocytes
A/Reference number: A49047; MUID:92387224; PMID:1516616
A/Accession: B49047
A/Status: preliminary
A/Molecule type: nucleic acid
A/Residues: 1-108 <VIC>
A/Experimental source: thymic B lymphocytes
A/Note: sequence extracted from NCBI backbone (NCBIN:113208, NCBI:113209)
C/Superfamily: Immunoglobulin V region; immunoglobulin homology
F/16-90/Domain: immunoglobulin homology <IMM>

Query Match 87.7%; Score 476; DB 2; Length 108;
Best Local Similarity 89.4%; Pred. No. 2.4e-35;
Matches 93; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 2 MTQSPSSLSASVGDRTVITTCRASQSIIRYLNWYQHKRGKAPKLLIHFTASSLSQGVPSRFS 61
DB 4 MTQSPSSLSASVGDRTVITTCRASQSIIRYLNWYQHKRGKAPKLLIHFTASSLSQGVPSRFS 63
QY 62 GSVSGTDFLTITSLQPEDFATYCCOQSYTTPYTFGGTKLQIK 105
DB 64 GSVSGTDFLTITSLQPEDFATYCCOQSYTTPYTFGGTKLQIK 107

RESULT 6

S31978

Ig kappa chain - human (fragment)

C/Species: Homo sapiens (man)
C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C/Accession: S31978
R/Portolano, S.; Chazenbalk, G.D.; Hutchison, S.J.; McLachlan, S.M.; Rapoport, B.
Submitted to the EMBL Data Library, June 1992
A/Description: Lack of promiscuity in autoantigen-specific H and L chain combinations as
A/Reference number: S31977.
A/Accession: S31978
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-109 <PDR>
A/Cross-references: EMBL:Z15074, NID:G38487, PIRN:CA178793.1, PID:G38488
C/Superfamily: Immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/16-90/Domain: immunoglobulin homology <IMM>

Query Match 87.3%; Score 474; DB 2; Length 109;
Best Local Similarity 86.7%; Pred. No. 3.6e-35;
Matches 91; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 1 VMTQSPSSLSASVGDRTVITTCRASQSIIRYLNWYQHKRGKAPKLLIHFTASSLSQGVPSRFS 60
DB 3 VMTQSPSSLSASVGDRTVITTCRASQSIIRYLNWYQHKRGKAPKLLIHFTASSLSQGVPSRFS 62
QY 61 GSVSGTDFLTITSLQPEDFATYCCOQSYTTPYTFGGTKLQIK 105
DB 63 GSVSGTDFLTITSLQPEDFATYCCOQSYTTPYTFGGTKLQIK 107

RESULT 7

S47182

Ig kappa chain - human

C/Species: Homo sapiens (man)
C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C/Accession: S47182

R/McIntosh, R.S.; Tandon, N.; Metcalfe, R.A.; Weetman, A.P.
submitted to the EMBL Data Library, June 1994
C/Keywords: heterotrimer; immunoglobulin
F/16-90/Domain: immunoglobulin autoantibodies from patient

A/Reference number: S47181

A/Accession: S47182

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-108 <MC1>

A/Cross-references: EMBL:X79786; NID:G506422; PIDN:CAA56182.1; PID:G506423

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotrimer; immunoglobulin

F/16-90/Domain: immunoglobulin homology <IMM>

Query Match 86.9%; Score 472; DB 2; Length 108;
Best Local Similarity 88.5%; Pred. No. 5.4e-35;
Matches 92; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 2 MTQSPSSLSASVGDRTVITCRASQSIIRYLNWYQHKPKAPKLLIHTASLSQGVPSRFS 61

Db 4 LTQSPSSLSASVGDRTVITCRASQSIIRYLNWYQHKPKAPKLLIHTASLSQGVPSRFS 63

QY 62 GSVSGTDFLTITISLQPEDFATYCCQSYTTPYTFGGTKLQIK 105

Db 64 GSGSGTDFLTITISLQPEDFATYCCQSYTTPYTFGGTKLQIK 107

RESULT 8

S44122

Ig kappa chain V region - human

C/Species: Homo sapiens (man)

C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-May-2001

C/Accession: S44122

R/Hawkins, R.E.; Zhu, D.; Ovecka, M.; Winter, G.; Hamlin, T.J.; Stevenson, F.K.
submitted to the EMBL Data Library, March 1994

A/Description: idiotype vaccination against human B-cell lymphoma: rescue of variable

A/Reference number: S44105

A/Accession: S44122

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-108 <HAW>

A/Cross-references: EMBL:Z31390; NID:G472976; PIDN:CAA83265.1; PID:G940533

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotrimer; immunoglobulin

F/16-90/Domain: immunoglobulin homology <IMM>

Query Match 85.6%; Score 465; DB 2; Length 108;
Best Local Similarity 87.5%; Pred. No. 2.3e-34;
Matches 91; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 2 MTQSPSSLSASVGDRTVITCRASQSIIRYLNWYQHKPKAPKLLIHTASLSQGVPSRFS 61

Db 4 MTQSPSSLSASVGDRTVITCRASQSIIRYLNWYQHKPKAPKLLIHTASLSQGVPSRFS 63

QY 62 GSVSGTDFLTITISLQPEDFATYCCQSYTTPYTFGGTKLQIK 105

Db 64 GSGSGTDFLTITISLQPEDFATYCCQSYTTPYTFGGTKLQIK 107

RESULT 9

S31979

Ig kappa chain - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000

C/Accession: S31979

R/Portolano, S.; Chazenbalk, G.D.; Hutchison, S.J.; McLachlan, S.M.; Rapoport, B.
submitted to the EMBL Data Library, June 1992

A/Description: Lack of promiscuity in autoantigen-specific H and L chain combinations as

A/Reference number: S31977

A/Accession: S31979

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-109 <POR>

A/Cross-references: EMBL:Z15075; NID:G38489; PIDN:CAA78784.1; PID:G38490

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotrimer; immunoglobulin

F/16-90/Domain: immunoglobulin homology <IMM>

Query Match 84.9%; Score 461; DB 2; Length 109;
Best Local Similarity 83.8%; Pred. No. 5.1e-34;
Matches 88; Conservative 11; Mismatches 6; Indels 0; Gaps 0;

QY 1 VMTQSPSSLSASVGDRTVITCRASQSIIRYLNWYQHKPKAPKLLIHTASLSQGVPSRFS 60

Db 3 VMTQSPSSLSASVGDRTVITCRASQSIIRYLNWYQHKPKAPKLLIHTASLSQGVPSRFS 62

QY 61 GSVSGTDFLTITISLQPEDFATYCCQSYTTPYTFGGTKLQIK 105

Db 63 GSGSGTDFLTITISLQPEDFATYCCQSYTTPYTFGGTKLQIK 107

RESULT 10

S31977

Ig kappa chain - human

C/Species: Homo sapiens (man)

C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Mar-2001

C/Accession: S31977

R/Portolano, S.; Chazenbalk, G.D.; Hutchison, S.J.; McLachlan, S.M.; Rapoport, B.
submitted to the EMBL Data Library, June 1992

A/Description: Lack of promiscuity in autoantigen-specific H and L chain combinations as

A/Reference number: S31977

A/Accession: S31977

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-108 <POR>

A/Cross-references: EMBL:Z15073

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotrimer; immunoglobulin

F/16-90/Domain: immunoglobulin homology <IMM>

Query Match 84.7%; Score 460; DB 2; Length 108;
Best Local Similarity 87.6%; Pred. No. 6.2e-34;
Matches 92; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

QY 1 VMTQSPSSLSASVGDRTVITCRASQSIIRYLNWYQHKPKAPKLLIHTASLSQGVPSRFS 60

Db 3 VMTQSPSSLSASVGDRTVITCRASQSIIRYLNWYQHKPKAPKLLIHTASLSQGVPSRFS 62

QY 61 GSVSGTDFLTITISLQPEDFATYCCQSYTTPYTFGGTKLQIK 105

Db 63 GSGSGTDFLTITISLQPEDFATYCCQSYTTPYTFGGTKLQIK 107

RESULT 11

S52793

Ig kappa chain V region - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 19-May-1995 #sequence_revision 03-Aug-1995 #text_change 21-Jan-2000

C/Accession: S52793

R/Rocca, A.; Khamilchi, A.A.; Touchard, G.; Mougenot, B.; Ronco, P.; Denoroy, L.; Deret,
submitted to the EMBL Data Library, March 1995

A/Description: Light chain V region gene usage restriction and peculiarities in myeloma-

A/Reference number: S52789

A/Accession: S52793

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-129 <ROC>

A/Cross-references: EMBL:X85997; NID:G758600; PIDN:CAA59989.1; PID:G758601

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotrimer; immunoglobulin

F/38-112/Domain: immunoglobulin homology <IMM>

Query Match 84.5%; Score 459; DB 2; Length 129;
Best Local Similarity 84.6%; Pred. No. 9.1e-34;
Matches 88; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

QY 2 MTQSPSSLSASVGDRTVITCRASQSIIRYLNWYQHKPKAPKLLIHTASLSQGVPSRFS 61

Db 26 MTQSPSSLASVGDRTVITCRASQNIISYLNWYQOKGKAPKLIHTTASSLSQGVPSRFV 85
|||
QY 62 GSVSGTDFLTITSSLOPEDPATYTCQOSYTPPTFGGCTKLOIK 105
|||
Db 86 GSGSGTDFLTITSSLOPEDPATYTCQOSYTPPTFGGCTKLOIK 129
|||

RESULT 12

K1HWK
Ig kappa chain precursor V-1 region (Walker) - human
C/Species: Homo sapiens (man)
C/Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 21-Jan-2000
C/Accession: A01883
R/Klobeck, H.G.; Combrat, G.; Zachau, H.G.
Nucleic Acids Res. 12, 6995-7006, 1984
A/Title: Immunoglobulin genes of the kappa light chain type from two human lymphoid cell
A/Reference number: A93534; MUID:85014148; PMID:6091049
A/Accession: A01883
A/Molecule type: DNA
A/Residues: 1-129 <KLO>
A/Note: the sequence was determined from the differentiated gene
C/Genetics:
A/Gene: GDB:IGKV1
A/Cross-references: GDB:136264
A/Map position: 2p12-2p12
C/Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as Iga and Igm, the subunits associate into 1d
C/Superfamily: Immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/1-22/Domain: signal sequence #status predicted <SIG>
F/23-129/Product: Ig kappa chain V-1 region (Walker) #status predicted <MAT>
F/23-45/Region: framework 1
F/38-112/Domain: immunoglobulin homology <IMM>
F/46-56/Region: complementarity-determining 1
F/57-71/Region: framework 2
F/72-78/Region: complementarity-determining 2
F/79-110/Region: framework 3
F/111-119/Region: complementarity-determining 3
F/120-129/Region: framework 4
F/45-110/Disulfide bonds: #status predicted

Query Match 84.3%; Score 458; DB 1; Length 129;
Best Local Similarity 87.5%; Pred. No. 1,1e-33;
Matches 91; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

QY 2 MTQSPSSLASVGDRTVITCRASQNIISYLNWYQOKGKAPKLIHTTASSLSQGVPSRF 61
|||
Db 26 MTQSPSSLASVGDRTVITCRASQNIISYLNWYQOKGKAPKLIHTTASSLSQGVPSRF 85
|||
QY 62 GSVSGTDFLTITSSLOPEDPATYTCQOSYTPPTFGGCTKLOIK 105
|||
Db 86 GSGSGTDFLTITSSLOPEDPATYTCQOSYTPPTFGGCTKLOIK 129
|||

RESULT 13

K1HND
Ig kappa chain V-1 region (Dee) - human (tentative sequence)
C/Species: Homo sapiens (man)
C/Date: 24-Apr-1994 #sequence_revision 24-Apr-1984 #text_change 31-Mar-2000
C/Accession: A01865
R/Milstein, C.P.; Deverson, E.V.
Biochem. J. 123, 945-958, 1971
A/Title: The amino acid sequence of a human kappa light chain.
A/Reference number: A01865; MUID:7205133; PMID:5124396
A/Accession: A01865
A/Molecule type: protein
A/Residues: 1-108 <MIT>
A/Note: the C region of this chain as the Inv (3) marker
C/Genetics:
A/Gene: GDB:IGKV1
A/Cross-references: GDB:136264
A/Map position: 2p12-2p12

C/Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as Iga and Igm, the subunits associate into 1d
C/Superfamily: Immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer
F/16-90/Domain: immunoglobulin homology <IMM>
F/23-86/Disulfide bonds: #status predicted

Query Match 84.2%; Score 457; DB 1; Length 108;
Best Local Similarity 84.5%; Pred. No. 1,1e-33;
Matches 87; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 2 MTQSPSSLASVGDRTVITCRASQNIISYLNWYQOKGKAPKLIHTTASSLSQGVPSRF 61
|||
Db 4 MTQSPSSLASVGDRTVITCRASQNIISYLNWYQOKGKAPKLIHTTASSLSQGVPSRF 63
|||
QY 62 GSVSGTDFLTITSSLOPEDPATYTCQOSYTPPTFGGCTKLOIK 104
|||
Db 64 GSGSGTDFLTITSSLOPEDPATYTCQOSYTPPTFGGCTKLOIK 106
|||

RESULT 14

S31980
Ig kappa chain - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C/Accession: S31980; S32000
R/Portiano, S.; Chazebal, G.D.; Hutchison, S.J.; McLachlan, S.M.; Rapoport, B.
submitted to the EMBL Data Library, June 1992
A/Description: Lack of promiscuity in autoantigen-specific H and L chain combinations as
A/Reference number: S31977
A/Accession: S31980
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-109 <POR>
A/Cross-references: EMBL:Z15076; NID:q38491; PTDN:CAA78785.1; PTD:q38492; EMBL:Z15083; N
C/Superfamily: Immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/16-90/Domain: immunoglobulin homology <IMM>

Query Match 84.2%; Score 457; DB 2; Length 109;
Best Local Similarity 82.9%; Pred. No. 1,2e-33;
Matches 87; Conservative 12; Mismatches 6; Indels 0; Gaps 0;

QY 1 VMTQSPSSLASVGDRTVITCRASQNIISYLNWYQOKGKAPKLIHTTASSLSQGVPSRF 60
|||
Db 3 VMTQSPSSLASVGDRTVITCRASQNIISYLNWYQOKGKAPKLIHTTASSLSQGVPSRF 62
|||
QY 61 GSVSGTDFLTITSSLOPEDPATYTCQOSYTPPTFGGCTKLOIK 105
|||
Db 63 GSGSGTDFLTITSSLOPEDPATYTCQOSYTPPTFGGCTKLOIK 107
|||

RESULT 15

S19674
Ig kappa chain V region (clone alpha-TEL9) - human
C/Species: Homo sapiens (man)
C/Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 20-Jun-2000
C/Accession: S19674
R/Marke, J.D.; Hoogenboom, H.R.; Bonner, T.P.; McCafferty, J.; Griffiths, A.D.; Winter, J.
Mol. Biol. 222, 581-597, 1991
A/Title: By-passing immunization. Human antibodies from V-gene libraries displayed on ph
A/Reference number: S19663; MUID:92085276; PMID:1748994
A/Accession: S19674
A/Molecule type: mRNA
A/Residues: 1-108 <MAR>
A/Cross-references: EMBL:X61642; NID:q37860; PTDN:CAA3923.1; PTD:q1335386
C/Superfamily: Immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/16-90/Domain: immunoglobulin homology <IMM>

Query Match 84.0%; Score 456; DB 2; Length 108;
Best Local Similarity 84.8%; Pred. No. 1,4e-33;
Matches 89; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

us-09-147-443d-60.rpr

[illegible]

Search completed: January 22, 2004, 11:53:45
Job time : 15.1522 secs

Matches 91; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

QY 2 MTGSPSSLSASVGDRTVITTCRASQSIIRYLMWYQHKRGKAPKLIHTASSLSQGVPSRFS 61
 DB 26 MTGSPSSLSASVGDRTVITTCRASQSIIRYLMWYQHKRGKAPKLIHTASSLSQGVPSRFS 85

QY 62 GSVSGTDFLTITISLQPEDPATYTCQOSYTPPTFGGCTKQIK 105
 DB 86 GSGSGTDFLTITISLQPEDPATYTCQOSYTPPTFGGCTKLEIK 129

RESULT 2
 KVI0_HUMAN STANDARD; PRT; 108 AA.
 AC P01607;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 15-JUL-1986 (Rel. 01, Last sequence update)
 DE Ig kappa chain V-I region DEE.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NC NCB1_TaxID=9606;
 RN [1]
 RP MEDLINE=72053133; PubMed=5124396;
 RA Miletich C.P., Deverson E.V.;
 RT "The amino acid sequence of a human kappa light chain.";
 RL Biochem. J. 123:945-958(1971).
 CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
 DR HSP: P01607; IREI.
 DR GO: GO:0005576; C:extracellular; NAS.
 DR GO: GO:0003823; F:antigen binding activity; NAS.
 DR GO: GO:0006955; P:immune response; NAS.
 DR InterPro: IPR007110; Ig_Like.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_V.
 DR Pfam: PF00047; Ig_1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KW Immunoglobulin V region.
 KW DOMAIN 1 23 FRAMEWORK-1.
 FT DOMAIN 1 23 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 35 49 FRAMEWORK-2.
 FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 57 88 FRAMEWORK-3.
 FT DOMAIN 89 97 FRAMEWORK-4.
 FT DOMAIN 98 107 COMPLEMENTARITY-DETERMINING-3.
 FT DISULFID 23 88 BY SIMILARITY.
 FT NON_TER 108 108
 SQ SEQUENCE 108 AA; 11661 MW; BDD6B3500171B51 CRC64;

Query Match 84.2%; Score 457; DB 1; Length 108;
 Best Local Similarity 84.5%; Pred. No. 2.4e-40;
 Matches 87; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 2 MTGSPSSLSASVGDRTVITTCRASQSIIRYLMWYQHKRGKAPKLIHTASSLSQGVPSRFS 61
 DB 4 MTGSPSSLSASVGDRTVITTCRASQSIIRYLMWYQHKRGKAPKLIHTASSLSQGVPSRFS 63

QY 62 GSVSGTDFLTITISLQPEDPATYTCQOSYTPPTFGGCTKQIK 104
 DB 64 GSGSGTDFLTITISLQPEDPATYTCQOSYTPPTFGGCTKQIK 106

RESULT 3
 KVI0_HUMAN STANDARD; PRT; 108 AA.
 AC P01607;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Ig kappa chain V-I region Hau.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NC NCB1_TaxID=9606;
 RN [1]
 RP MEDLINE=71032830; PubMed=4097974;
 RA Watanabe S., Hilschmann N.;
 RT "The primary structure of a monoclonal kappa-type immunoglobulin L-chain of subgroup I (Bence-Jones Protein Hau): subdivision within subgroups.";
 RL Hoppe-Seyler's Z. Physiol. Chem. 351:1291-1295(1970).
 CC -1- MISCELLANEOUS: THIS IS A BENICE-JONES PROTEIN.
 DR HSP: P00362; IWTU.
 DR GO: GO:0005576; C:extracellular; NAS.
 DR GO: GO:0003823; F:antigen binding activity; NAS.
 DR GO: GO:0006955; P:immune response; NAS.
 DR InterPro: IPR007110; Ig_Like.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_V.
 DR Pfam: PF00047; Ig_1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KW Immunoglobulin V region; Bence-Jones protein.
 KW DOMAIN 1 23 FRAMEWORK-1.
 FT DOMAIN 1 23 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 35 49 FRAMEWORK-2.
 FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 57 88 FRAMEWORK-3.
 FT DOMAIN 89 97 FRAMEWORK-4.
 FT DISULFID 23 88 BY SIMILARITY.
 FT NON_TER 108 108
 SQ SEQUENCE 108 AA; 11671 MW; 08D3A61608D0618 CRC64;

Query Match 83.2%; Score 452; DB 1; Length 108;
 Best Local Similarity 83.7%; Pred. No. 7.9e-40;
 Matches 87; Conservative 9; Mismatches 8; Indels 0; Gaps 0;

QY 2 MTGSPSSLSASVGDRTVITTCRASQSIIRYLMWYQHKRGKAPKLIHTASSLSQGVPSRFS 61
 DB 4 MTGSPSSLSASVGDRTVITTCRASQSIIRYLMWYQHKRGKAPKLIHTASSLSQGVPSRFS 63

QY 62 GSVSGTDFLTITISLQPEDPATYTCQOSYTPPTFGGCTKQIK 105
 DB 64 GSGSGTDFLTITISLQPEDPATYTCQOSYTPPTFGGCTKQIK 107

RESULT 4
 KVI0_HUMAN STANDARD; PRT; 108 AA.
 AC P01607;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Ig kappa chain V-I region Rel.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NC NCB1_TaxID=9606;
 RN [1]
 RP MEDLINE=76023758; PubMed=809329;
 RA Palm W., Hilschmann N.;
 RT "The primary structure of a crystalline monoclonal immunoglobulin kappa-type L-chain, subgroup I (Bence-Jones protein Rel); isolation and characterization of the tryptic peptides; the complete amino acid sequence of the protein; a contribution to the elucidation of the three-dimensional structure of antibodies, in particular their combining site.";

RL Hoppe-Seyler's Z. Physiol. Chem. 356:167-191(1975).
 RN [2]
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
 RX MEDLINE=76039668; PubMed=1182133;
 RA Bpp O., Latman E.E., Schiffer M., Huber R., Palm W.;
 RT "The molecular structure of a dimer composed of the variable portions
 of the Bence-Jones protein RFI refined at 2.0-A resolution.";
 RL Biochemistry 14:4943-4952(1975).
 CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
 CC MARKER.
 CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
 DR PIR; A91663; KIHURE.
 DR PDB; 1REI; 17-FEB-84.
 DR PDB; 1AR2; 12-NOV-97.
 DR PDB; 1BW2; 29-DEC-99.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:000823; F:antigen binding activity; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG_LIKE; 1.
 KW Immunoglobulin V region; Bence-Jones protein; 3D-structure.
 FT DOMAIN 1 23 FRAMEWORK-1.
 FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 35 49 FRAMEWORK-2.
 FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 57 88 FRAMEWORK-3.
 FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
 FT DOMAIN 98 107 FRAMEWORK-4.
 FT DISULFID 23 88
 FT STRAND 4 7
 FT STRAND 10 13
 FT TURN 15 16
 FT STRAND 19 25
 FT TURN 30 31
 FT STRAND 33 38
 FT TURN 40 41
 FT STRAND 44 49
 FT TURN 50 52
 FT STRAND 53 54
 FT TURN 56 57
 FT TURN 60 61
 FT STRAND 62 67
 FT TURN 68 69
 FT STRAND 70 75
 FT HELIX 80 82
 FT STRAND 85 90
 FT STRAND 97 98
 FT STRAND 102 106
 FT NON TER 108
 SQ SEQUENCE 108 AA; 11902 MW; 9E8143E1188BCE2A CRC64;
 Query Match 82.3%; Score 447; DB 1; Length 108;
 Best Local Similarity 83.5%; Pred. No. 2.6e-39;
 Matches 86; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE 15-kappa chain V-I region OI.
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 ON NCBI_TaxID=9606;
 RX MEDLINE=70201507; PubMed=5447531;
 RA Kohler H., Shimizu A., Paul C., Putnam F.W.;
 RT "Macroglobulin structure: variable sequence of light and heavy
 chains";
 RL Science 169:56-59(1970).
 CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S
 CC MACROGLOBULIN.
 DR PIR; A01872; KIHUCU.
 DR HSSP; P01607; 1REI.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:000823; F:antigen binding activity; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG_LIKE; 1.
 KW Immunoglobulin V region.
 FT DOMAIN 1 23 FRAMEWORK-1.
 FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 35 49 FRAMEWORK-2.
 FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 57 88 FRAMEWORK-3.
 FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
 FT DOMAIN 98 107 FRAMEWORK-4.
 FT DISULFID 23 88 BY SIMILARITY.
 FT NON TER 108
 SQ SEQUENCE 108 AA; 11777 MW; 8283DA42A105827E CRC64;
 Query Match 79.9%; Score 434; DB 1; Length 108;
 Best Local Similarity 73.1%; Pred. No. 5.6e-38;
 Matches 76; Conservative 18; Mismatches 10; Indels 0; Gaps 0;

QY 2 MTQSPSSLSASVGDRTITCRASQSIIRYLNWYQHKPKAPKLLIHTASSLSQGVSPSRFS 61
 DB 4 MTQSPSSLSASVGDRTITCRASQSIIRYLNWYQHKPKAPKLLIHTASSLSQGVSPSRFS 63
 QY 62 GSVSGTDFLTITSSLOPEDPATYTCQOSYTPPTFGQGTLOIK 104
 DB 64 GSGSGTDFLTITSSLOPEDPATYTCQOSYTPPTFGQGTLOIK 106

RESULT 6
 ID KV1V HUMAN STANDARD; PRT; 108 AA.
 AC P04430;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE 15-kappa chain V-I region BAN.
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 ON NCBI_TaxID=9606;
 RX MEDLINE=86174817; PubMed=3083240;
 RA Dmulet F.E., O'Connor T.P., Benson M.D.;
 RT "Polymorphism in a kappa I primary (AL) amyloid protein (BAN).";
 RL Mol. Immunol. 23:73-78(1986).
 DR PIR; A01878; KIHUEN.
 DR HSSP; P80362; 1WTL.

DR GO: GO:0005576; C:extracellular; NAS.
 DR GO: GO:0003823; F:antigen binding activity; NAS.
 DR GO: GO:0006955; P:immune response; NAS.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_v.
 DR Pfam: PF00047; Ig; 1.
 DR SMART: SM00406; IGV; 1.
 DR PROSITE: PSS0835; IG LIKE; 1.
 DR Immunoglobulin V region; Amyloid.
 KW DOMAIN 1 23 FRAMEWORK-1.
 FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 35 49 FRAMEWORK-2.
 FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 57 88 FRAMEWORK-3.
 FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
 FT DOMAIN 98 107 FRAMEWORK-4.
 FT DISULFID 23 88 BY SIMILARITY.
 FT NON TER 109 109
 SQ SEQUENCE 108 AA; 11840 MW; CD3FD944FE96FD37 CRC64;

Query Match 79.4%; Score 431; DB 1; Length 108;
 Best Local Similarity 79.8%; Pred. No. 1.1e-37;
 Matches 83; Conservative 9; Mismatches 12; Indels 0; Gaps 0;

QY 2 MTQSPSSLSASVGDRTVITTCRASQSIIRLYNMYQKRGKAPKLLIFDTSNLSQSGVSPRFS 61
 DB 4 LTQSPSSLSASVGRVITTCRASQSYVNYVAMPQKRGKAPKLLIFDTSNLSQSGVSPNFT 63

QY 62 GSVSGTDFLTITSLQPEDPATYCCQOSYTPPYFGGKTKQIK 105
 DB 64 GSGSGTDFLTITSLQPEDPATYCCQYNSGYPTFGGKTVQIK 107

RESULT 7
 KVI1_HUMAN STANDARD; PRT; 109 AA.
 ID KVI1_HUMAN
 AC P01612;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE IG kappa chain V-I region Mv.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI_TaxID=9606;
 RX MEDLINE=63081018; PubMed=6816713;
 RA Bulter M., Linke R.P.;
 RT "Primary structure of the variable part of an amyloidogenic Bence-Jones protein (Mv). An unusual insertion in the third hypervariable region of a human kappa-immunoglobulin light chain."
 RT Hoppe-Seyler's Z. Physiol. Chem. 363:1347-1358(1982).
 CC -1- MISCELLANEOUS: ANOTHER FORM THAT LACKED RESIDUES 1-3 WAS ALSO FOUND.
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
 CC PIR: A01879; KIHUUV.
 DR HSP; P80362; IMTL.
 DR GO: GO:0005576; C:extracellular; NAS.
 DR GO: GO:0003823; F:antigen binding activity; NAS.
 DR GO: GO:0006955; P:immune response; NAS.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003006; Ig_MHC.
 DR Pfam: PF00047; Ig; 1.
 DR SMART: SM00406; IGV; 1.
 DR PROSITE: PSS0835; IG LIKE; 1.
 DR Immunoglobulin V region; Bence-Jones protein.
 KW DOMAIN 1 23 FRAMEWORK-1.
 FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 35 49 FRAMEWORK-2.
 FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
 FT DISULFID 23 88 BY SIMILARITY.

FT DOMAIN 57 88 FRAMEWORK-3.
 FT DOMAIN 89 98 COMPLEMENTARITY-DETERMINING-3.
 FT DOMAIN 99 108 FRAMEWORK-4.
 FT DISULFID 23 88 BY SIMILARITY.
 FT NON TER 109 109
 SQ SEQUENCE 109 AA; 11870 MW; B6ABF451D55F5A0 CRC64;

Query Match 79.3%; Score 430.5; DB 1; Length 109;
 Best Local Similarity 81.9%; Pred. No. 1.3e-37;
 Matches 86; Conservative 4; Mismatches 14; Indels 1; Gaps 1;

QY 2 MTQSPSSLSASVGDRTVITTCRASQSIIRLYNMYQKRGKAPKLLIFDTSNLSQSGVSPRFS 61
 DB 4 MTQSPSSLSASVGRVITTCRASQSYVNYVAMPQKRGKAPKLLIFDTSNLSQSGVSPRFS 63

QY 62 GSVSGTDFLTITSLQPEDPATYCCQOSYTPPYFGGKTKQIK 105
 DB 64 GSGSGTDFLTITSLQPEDPATYCCQYNSGYPTFGGKTVQIK 108

RESULT 8
 KVI1_HUMAN STANDARD; PRT; 108 AA.
 ID KVI1_HUMAN
 AC P01594;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE IG kappa chain V-I region AU.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI_TaxID=9606;
 RX MEDLINE=72189444; PubMed=5028201;
 RA Schiechl H., Hilschmann N.;
 RT "Rule of antibody structure. The primary structure of a monoclonal immunoglobulin L-chain of the kappa-type, subgroup I (Bence-Jones protein Au)."
 RT Hoppe-Seyler's Z. Physiol. Chem. 353:345-370(1972).
 CC [2]
 RX X-RAY CRYSTALLOGRAPHY.
 RX MEDLINE=77022433; PubMed=1234024;
 RA Fehlgammer H., Schiffer M., Epp O., Colman P.M., Lattman E.E.,
 RA Schwager P., Steigemann W., Schramm H.J.;
 RT "The structure determination of the variable portion of the Bence-Jones protein Au."
 RT Biophys. Struct. Mech. 1:139-146(1975).
 CC -1- MISCELLANEOUS: THE STRUCTURE OF THE V REGION WAS DETERMINED BY MOLECULAR REPLACEMENT METHODS USING THE KNOWN STRUCTURE OF THE V REGION OF THE KAPPA CHAIN REI.
 CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
 CC PIR: A91653; KIHUUV.
 DR PDB: 1UV5; 30-JAN-02.
 DR GO: GO:0005576; C:extracellular; NAS.
 DR GO: GO:0003823; F:antigen binding activity; NAS.
 DR GO: GO:0006955; P:immune response; NAS.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003006; Ig_MHC.
 DR Pfam: PF00047; Ig; 1.
 DR SMART: SM00406; IGV; 1.
 DR PROSITE: PSS0835; IG LIKE; 1.
 DR Immunoglobulin V region; Bence-Jones protein; 3D-structure.
 KW DOMAIN 1 23 FRAMEWORK-1.
 FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 35 49 FRAMEWORK-2.
 FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 57 88 FRAMEWORK-3.
 FT DOMAIN 89 97 FRAMEWORK-4.
 FT DOMAIN 98 107 FRAMEWORK-4.
 FT DISULFID 23 88 BY SIMILARITY.

FT NON TER 108 108
SQ SEQUENCE 108 AA; 11939 MW; E801187EB6F6B9 CRC64;

Query Match 77.2%; Score 419; DB 1; Length 108;
Best Local Similarity 78.8%; Pred. No. 2e-36;
Matches 82; Conservative 7; Mismatches 15; Indels 0; Gaps 0;

QY 2 MTQSPSSLSASVGDRTVITTCRASQSIIRYINWYQHKPKAKPKLLIHTASSLSQSGVPSRFS 61
DB 4 MTQSPSSLSASVGDRTVITTCRASQSDIDYINWYQHKPKAKPKLLIHTASSLSQSGVPSRFS 63

QY 62 GSVSGDFTLTISLQPEDPATYTCQOSYTPYTFGCGTKLOIK 105
DB 64 GSGSGTBTFTLTISLQPEDPATYTCQOYDYLPMTFGGTVVDIK 107

RESULT 9

KV1K_HUMAN STANDARD; PRT; 108 AA.

ID KV1K_HUMAN STANDARD; PRT; 108 AA.
AC P01603;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region Ka.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;

SEQUENCE.
RA MEDLINE=76189985; PubMed=818073;
RA Shindoda T.;
RT "Comparative structural studies on the light chains of human immunoglobulins. I. Protein Ka with the Inv(3) allocyclic marker."
RL J. Biochem. 77:1277-1296(1975).
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR PIR; A01869; KIHUKA.
DR HSSP; P80362; 1MTL.

DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS50835; IG_LIKE; 1.

KW Immunoglobulin V region; Bence-Jones protein.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 FRAMEWORK-2.
FT DOMAIN 35 49 FRAMEWORK-3.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 107 FRAMEWORK-4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON TER 108 108
SQ SEQUENCE 108 AA; 11900 MW; 768839FBD5A2F4B CRC64;

Query Match 77.0%; Score 418; DB 1; Length 108;
Best Local Similarity 72.1%; Pred. No. 2.5e-36;
Matches 75; Conservative 15; Mismatches 14; Indels 0; Gaps 0;

QY 2 MTQSPSSLSASVGDRTVITTCRASQSIIRYINWYQHKPKAKPKLLIHTASSLSQSGVPSRFS 61
DB 4 MTQSPSSLSASVGDRTVITTCRASQSVSYINWYQHKPKAKPKLLIHTASSLSQSGVPSRFS 63
QY 62 GSVSGDFTLTISLQPEDPATYTCQOSYTPYTFGCGTKLOIK 105
DB 64 GSGSGTBTFTLTISLQPEDPATYTCQOYDYLPMTFGGTVVDIK 107

RESULT 10
KV1S_HUMAN STANDARD; PRT; 108 AA.

ID KV1S_HUMAN STANDARD; PRT; 108 AA.
AC P01611;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region Wes.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;

SEQUENCE.
RA MEDLINE=81092279; PubMed=6778806;
RA Kratzin H., Yang C., Krusche J.U., Hillechmann N.;
RT "Preparative separation of the tryptic hydrolyzate of a protein by high-pressure liquid chromatography. The primary structure of a monoclonal L-chain of k-type, subgroup I (Bence-Jones protein Wes)."
RL Hoppe-Seyler's Z. Physiol. Chem. 361:1591-1598(1980).
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.

DR PIR; A01877; KIHWS.
DR HSSP; P80362; 1MTL.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 FRAMEWORK-2.
FT DOMAIN 35 49 FRAMEWORK-3.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 107 FRAMEWORK-4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON TER 108 108
SQ SEQUENCE 108 AA; 11608 MW; 782B14A649A60E45 CRC64;

Query Match 76.4%; Score 415; DB 1; Length 108;
Best Local Similarity 76.9%; Pred. No. 5e-36;
Matches 80; Conservative 12; Mismatches 12; Indels 0; Gaps 0;

QY 2 MTQSPSSLSASVGDRTVITTCRASQSIIRYINWYQHKPKAKPKLLIHTASSLSQSGVPSRFS 61
DB 4 MTQSPSSLSASVGDRTVITTCRASQSDISHLWYQKSGKPKLLIHTASSLSQSGVPSRFS 63

QY 62 GSVSGDFTLTISLQPEDPATYTCQOSYTPYTFGCGTKLOIK 105
DB 64 GSGSGTBTFTLTISLQPEDPATYTCQOAHSAVPLTFGGTVDIK 107

RESULT 11

KV1Y_HUMAN STANDARD; PRT; 108 AA.

ID KV1Y_HUMAN STANDARD; PRT; 108 AA.
AC P80362;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ig kappa chain V-I region MAT.

OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;

RP SEQUENCE, AND X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).

RX MEDLINE=95086080; PubMed=7993911;
 RA Huang D.-B., Chang C.-H., Ainsworth C., Bruenger A.T., Eultz M.,
 RA Solomon A., Stevens F.J., Schiffer M.;
 RT "Comparison of crystal structures of two homologous proteins:
 RT structural origin of altered domain interactions in immunoglobulin
 RT light-chain dimers.";
 RL Biochemistry 33:14848-14857(1994).
 RN [2]
 RP SEQUENCE OF 1-35.
 RX MEDLINE=81267384; PubMed=6167731;
 RA Stevens F.J., Westholm F.A., Panagiotopoulos N., Schiffer M.,
 RA Poppe R.A., Solomon A.;
 RT "Characterization and preliminary crystallographic data on the VL-
 RT related fragment of the human ki Bence Jones protein Wac.";
 RL J. Mol. Biol. 147:185-193(1991).
 CC -1- MISCELLANEOUS: THIS IS A BENICE-JONES PROTEIN.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding activity; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_MHC.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; Ig; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KM Immunoglobulin V region; Bence-Jones protein; 3D-structure.
 FT DOMAIN 1 23 FRAMEWORK-1.
 FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 35 49 FRAMEWORK-2.
 FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 57 88 FRAMEWORK-3.
 FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
 FT DOMAIN 98 107 FRAMEWORK-4.
 FT DISULFID 23 88 BY SIMILARITY.
 FT CONFLICT 30 31 TN -> SD (IN REF. 2).
 FT STRAND 4 7
 FT STRAND 10 13
 FT TURN 15 16
 FT STRAND 19 25
 FT TURN 30 31
 FT STRAND 33 38
 FT TURN 40 41
 FT STRAND 45 49
 FT TURN 50 52
 FT STRAND 53 54
 FT TURN 56 57
 FT TURN 60 61
 FT STRAND 62 67
 FT TURN 68 69
 FT STRAND 70 75
 FT HELIX 80 82
 FT STRAND 84 90
 FT STRAND 98 98
 FT STRAND 102 106
 FT NON_TER 108 108
 SQ SEQUENCE 108 AA; 11737 MW; D9D941B3F0FAE697 CRC64;
 Query Match 76.1%; Score 413; DB 1; Length 108;
 Best Local Similarity 76.9%; Pred. No. 8.1e-36;
 Matches 80; Conservative 9; Mismatches 15; Indels 0; Gaps 0;
 QY 2 MTQSPSSLSASVGDRTVITTCASQSIIRYLMWYQHKGAKKLIHTASSLSQGVPSRFS 61
 DB 4 MTQSPSSLSASVGDRTVITTCASQSIIRYLMWYQHKGAKKLIHTASSLSQGVPSRFS 63
 QY 62 GSVSGTDFLTITSLQPEDPATYTCQOSYTPYTFGGGTLOIK 105
 DB 64 GSGSGTDFLTITSLQPEDPATYTCQOSYTPYTFGGGTLOIK 107
 RESULT 12
 -KVIA_HUMAN

ID KVIA_HUMAN STANDARD; PRT; 108 AA.
 AC P01593;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE 15 kappa chain V-I region AG.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=69234734; PubMed=4893682;
 RA Titani K., Shinoda T., Putnam F.W.;
 RT "The amino acid sequence of a kappa type Bence-Jones protein. 3. The
 RT complete sequence and the location of the disulfide bridges.";
 RL J. Biol. Chem. 244:3550-3560(1969).
 CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding activity; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_MHC.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; Ig; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KM Immunoglobulin V region; Bence-Jones protein.
 FT DOMAIN 1 23 FRAMEWORK-1.
 FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 35 49 FRAMEWORK-2.
 FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 57 88 FRAMEWORK-3.
 FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
 FT DISULFID 23 88 FRAMEWORK-4.
 FT NON_TER 108 108
 SQ SEQUENCE 108 AA; 11992 MW; E3B3B246C18F0CAF CRC64;
 Query Match 75.9%; Score 412; DB 1; Length 108;
 Best Local Similarity 77.9%; Pred. No. 1e-35;
 Matches 81; Conservative 7; Mismatches 16; Indels 0; Gaps 0;
 QY 2 MTQSPSSLSASVGDRTVITTCASQSIIRYLMWYQHKGAKKLIHTASSLSQGVPSRFS 61
 DB 4 MTQSPSSLSASVGDRTVITTCASQSIIRYLMWYQHKGAKKLIHTASSLSQGVPSRFS 63
 QY 62 GSVSGTDFLTITSLQPEDPATYTCQOSYTPYTFGGGTLOIK 105
 DB 64 GSGSGTDFLTITSLQPEDPATYTCQOSYTPYTFGGGTLOIK 107
 RESULT 13
 ID KVIR_HUMAN STANDARD; PRT; 108 AA.
 AC P01610;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE 15 kappa chain V-I region WEA.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=63273707; PubMed=6410398;
 RA Gont F., Frangione B.;
 RT "Amino acid sequence of the Fv region of a human monoclonal IgM
 RT (protein WEA) with antibody activity against 3,4-pyruvylated

RT galactose in Klebsiella polysaccharides K30 and K33.";
 RL Proc. Natl. Acad. Sci. U.S.A. 80:4837-4841(1983).
 CC -1- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM A MONOCLONAL ANTIBODY
 AGAINST 3,4-PYRUVYLATED GALACTOSE AND ISOLATED FROM A PATIENT WITH
 CC WALDENSTROM'S MACROGLOBULINEMIA.
 DR PIR; A01876; KIHUWE.
 DR HSSP; P80362; 1WTU.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding activity; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 DR Immunoglobulin V region; Monoclonal antibody.
 KW DOMAIN 1 23 FRAMEWORK-1.
 FT DOMAIN 1 24 34 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 35 49 FRAMEWORK-2.
 FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 57 88 FRAMEWORK-3.
 FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
 FT DOMAIN 98 107 FRAMEWORK-4.
 FT DISULFID 23 88 BY SIMILARITY.
 FT NON TER 108 108
 SQ SEQUENCE 108 AA; 11840 MW; 9249B61F0945618C CRC64;
 Query Match 75.9%; Score 412; DB 1; Length 108;
 Best Local Similarity 77.9%; Pred. No. 1e-35;
 Matches 81; Conservative 9; Mismatches 14; Indels 0; Gaps 0;
 QY 2 MTQSPSSLSASVGDVDTTCRASQSIIRYLWYOHKRGKAPKLLHTASSLSQGVPSRFS 61
 DB 4 MTQSPSSLSASVGDVDTTCRASQSIIRYLWYOHKRGKAPKLLHTASSLSQGVPSRFS 63
 QY 62 GSVSGTDFLTLLISLOPEDFATYYCOOSYTPPYTFCGGTKLOIK 105
 DB 64 GSSSGTDFLTLLISLOPEDFATYYCOOSYTPPYTFCGGTKLOIK 107
 RESULT 14
 KVID_HUMAN STANDARD; PRT; 107 AA.
 AC P01596;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-I region CAR.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI_Taxid=9606;
 RX MEDLINE=75075135; Pubmed=4216454;
 RP SEQUENCE.
 RA Milstein C.P., Deverson E.V.;
 RT "Primary structure of kappa light chain from a human myeloma
 RT protein.";
 BU J. Biol. Chem. 49:377-391(1974).
 CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
 CC MARKER.
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
 DR PIR; A01864; KIHUAK.
 DR HSSP; P80362; 1WTU.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding activity; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR SMART; SM00406; IGV; 1.

DR PROSITE; PS50835; IG_LIKE; 1.
 KW Immunoglobulin V region; Glycoprotein.
 FT CARBOHYD 28 28 N-LINKED (GLCNAC. . .).
 FT NON TER 107 107
 SQ SEQUENCE 107 AA; 11703 MW; E1BF0D9844C3346 CRC64;
 Query Match 75.6%; Score 410.5; DB 1; Length 107;
 Best Local Similarity 76.9%; Pred. No. 1.5e-35;
 Matches 80; Conservative 12; Mismatches 11; Indels 1; Gaps 1;
 QY 2 MTQSPSSLSASVGDVDTTCRASQSIIRYLWYOHKRGKAPKLLHTASSLSQGVPSRFS 61
 DB 4 MTQSPSSLSASVGDVDTTCRASQSIIRYLWYOHKRGKAPKLLHTASSLSQGVPSRFS 63
 QY 62 GSVSGTDFLTLLISLOPEDFATYYCOOSYTPPYTFCGGTKLOIK 105
 DB 64 GSSSGTDFLTLLISLOPEDFATYYCOOSYTPPYTFCGGTKLOIK 106
 RESULT 15
 KVID_HUMAN STANDARD; PRT; 108 AA.
 AC P01604;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-I region Kue.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI_Taxid=9606;
 RX MEDLINE=79237924; Pubmed=112021;
 RA Bullitz M., Kley H.-P., Zeidler H.-U.;
 RT "The primary structure of the Bence-Jones protein Kue. The amino acid
 RT sequence of the variable part of a human L-chain of the kappa-type.";
 RT Hoppe-Sayler's Z. Physiol. Chem. 360:725-734(1979).
 CC -1- MISCELLANEOUS: THIS IS A BENICE-JONES PROTEIN.
 CC -1- MISCELLANEOUS: THIS IS A BENICE-JONES PROTEIN.
 DR PIR; A01870; KIHUKU.
 DR HSSP; P01607; 1REI.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding activity; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KW Immunoglobulin V region; Bence-Jones protein.
 FT DOMAIN 1 23 FRAMEWORK-1.
 FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 35 49 FRAMEWORK-2.
 FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 57 88 FRAMEWORK-3.
 FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
 FT DOMAIN 98 107 FRAMEWORK-4.
 FT DISULFID 23 88 BY SIMILARITY.
 FT NON TER 108 108
 SQ SEQUENCE 108 AA; 12127 MW; 906679A5D90EA898 CRC64;
 Query Match 75.5%; Score 410; DB 1; Length 108;
 Best Local Similarity 77.9%; Pred. No. 1.7e-35;
 Matches 81; Conservative 9; Mismatches 14; Indels 0; Gaps 0;
 QY 2 MTQSPSSLSASVGDVDTTCRASQSIIRYLWYOHKRGKAPKLLHTASSLSQGVPSRFS 61
 DB 4 MTQSPSSLSASVGDVDTTCRASQSIIRYLWYOHKRGKAPKLLHTASSLSQGVPSRFS 63
 QY 62 GSVSGTDFLTLLISLOPEDFATYYCOOSYTPPYTFCGGTKLOIK 105
 DB 64 GSSSGTDFLTLLISLOPEDFATYYCOOSYTPPYTFCGGTKLOIK 106

Thu Jan 22 12:05:07 2004

us-09-147-443d-60.rsp

Page 8

Db 64 GSGGTEFTLINSLOPPDPATYVCOQYSRYPYFGQTKLDIK 107

Search completed: January 22, 2004, 11:51:49
Job time : 10.1304 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 22, 2004, 11:42:41 ; Search time 31.5 Seconds
(without alignments)
860.175 Million cell updates/sec

Title: US-09-147-443D-60
Perfect score: 543
Sequence: 1 VMTQSPSSLSASVGRVIT.....COQSYTPYFGQGRQLQIK 105

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues
Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_23:*
1: sp archaea:*
2: sp bacteria:*
3: sp fungi:*
4: sp human:*
5: sp invertebrate:*
6: sp mammal:*
7: sp mhc:*
8: sp organelle:*
9: sp phage:*
10: sp plant:*
11: sp rodent:*
12: sp virus:*
13: sp vertebrate:*
14: sp unclassified:*
15: sp_rv1rus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|-----------|--------------------|
| 1 | 470 | 86.6 | 108 | 4 Q9UL77 | Q9UL77 homo sapien |
| 2 | 458.5 | 84.4 | 107 | 4 Q96SA9 | Q96SA9 homo sapien |
| 3 | 433.5 | 79.8 | 107 | 4 Q9UL81 | Q9UL81 homo sapien |
| 4 | 424 | 78.1 | 108 | 4 Q9UL70 | Q9UL70 homo sapien |
| 5 | 421 | 77.5 | 108 | 4 Q9UL79 | Q9UL79 homo sapien |
| 6 | 389 | 71.6 | 116 | 4 Q96PF6 | Q96PF6 homo sapien |
| 7 | 378 | 69.6 | 128 | 11 Q9QYF0 | Q9QYF0 mus musculu |
| 8 | 372 | 68.5 | 109 | 11 Q920E6 | Q920E6 mus musculu |
| 9 | 371 | 68.3 | 123 | 11 Q91WS9 | Q91WS9 mus musculu |
| 10 | 370 | 68.1 | 234 | 11 Q8RC62 | Q8RC62 mus musculu |
| 11 | 368 | 67.8 | 234 | 11 Q8VCP0 | Q8VCP0 mus musculu |
| 12 | 367 | 67.6 | 234 | 4 Q8NEK1 | Q8NEK1 homo sapien |
| 13 | 367 | 67.6 | 234 | 11 Q91WF8 | Q91WF8 mus musculu |
| 14 | 360 | 66.3 | 111 | 11 Q920E9 | Q920E9 mus musculu |
| 15 | 357 | 65.7 | 107 | 11 Q9ERZ9 | Q9ERZ9 mus musculu |
| 16 | 357 | 65.7 | 108 | 4 Q9UL83 | Q9UL83 homo sapien |

| ID | Score | Query Match | Length | ID | Description |
|----|-------|-------------|--------|-----------|---------------------|
| 17 | 355.5 | 65.5 | 109 | 4 Q9UL78 | Q9UL78 homo sapien |
| 18 | 348 | 64.1 | 214 | 11 Q9RIAS | Q9RIAS mus musculu |
| 19 | 344 | 63.4 | 108 | 11 Q8VJ10 | Q8VJ10 mus musculu |
| 20 | 340.5 | 62.7 | 109 | 4 Q9UL85 | Q9UL85 homo sapien |
| 21 | 340.5 | 62.7 | 114 | 11 Q8K1F1 | Q8K1F1 mus musculu |
| 22 | 339.5 | 62.5 | 112 | 11 Q8K1F3 | Q8K1F3 mus musculu |
| 23 | 338.5 | 62.3 | 109 | 4 Q9UL86 | Q9UL86 homo sapien |
| 24 | 336 | 61.9 | 107 | 11 Q9UL84 | Q9UL84 mus musculu |
| 25 | 334.5 | 61.6 | 112 | 11 Q8K1F2 | Q8K1F2 mus musculu |
| 26 | 332 | 61.1 | 127 | 11 Q925S9 | Q925S9 mus musculu |
| 27 | 331.5 | 61.0 | 238 | 11 Q9NM37 | Q9NM37 mus musculu |
| 28 | 330.5 | 60.9 | 134 | 11 Q8VDD0 | Q8VDD0 mus musculu |
| 29 | 325 | 59.9 | 99 | 11 Q9UL74 | Q9UL74 mus musculu |
| 30 | 324.5 | 59.8 | 241 | 11 Q921A6 | Q921A6 mus musculu |
| 31 | 322.5 | 59.4 | 106 | 5 Q9UL410 | Q9UL410 schistosoma |
| 32 | 321.5 | 59.2 | 238 | 11 Q8VCT6 | Q8VCT6 mus musculu |
| 33 | 320.5 | 59.0 | 239 | 4 Q8NEK0 | Q8NEK0 homo sapien |
| 34 | 314 | 57.8 | 103 | 11 Q9UL80 | Q9UL80 mus musculu |
| 35 | 313 | 57.6 | 101 | 11 Q9UL78 | Q9UL78 mus musculu |
| 36 | 312.5 | 57.6 | 112 | 11 Q8K1F0 | Q8K1F0 mus musculu |
| 37 | 312.5 | 57.6 | 239 | 11 Q8VCS5 | Q8VCS5 mus musculu |
| 38 | 306.5 | 56.4 | 235 | 11 Q91W12 | Q91W12 mus musculu |
| 39 | 305.5 | 56.3 | 239 | 4 Q8TCD0 | Q8TCD0 homo sapien |
| 40 | 304.5 | 56.1 | 239 | 11 Q8K0F8 | Q8K0F8 mus musculu |
| 41 | 303.5 | 55.9 | 104 | 11 Q9UL82 | Q9UL82 mus musculu |
| 42 | 301 | 55.4 | 97 | 11 Q9UL76 | Q9UL76 mus musculu |
| 43 | 299 | 55.1 | 114 | 4 Q9UL80 | Q9UL80 homo sapien |
| 44 | 294 | 54.1 | 234 | 11 Q8R028 | Q8R028 mus musculu |
| 45 | 291 | 53.6 | 109 | 6 Q9N0W5 | Q9N0W5 oryctolagus |

ALIGNMENTS

RESULT 1
Q9UL77 PRELIMINARY; PRT; 108 AA.
AC Q9UL77;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berner S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL: AF035037; AAD56273.1; -
DR HSSP: P01607; IREI.
DR InterPro: IPR007110; Ig_L-like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PSS0835; IG_LIKE; 1.
FT NON_TER
FT NON_TER
SQ SEQUENCE 108 AA; 11738 MW; C06681716C4D16F3 CRC64;

Query Match 86.6%; Score 470; DB 4; Length 108;
Best Local Similarity 87.5%; Pred. No. 3.2e-45;
Matches 91; Conservative 6; Mismatches 7; Indels 0; Gaps 0;
2 VMTQSPSSLSASVGRVITTCRASOSIIRYLMVYQHKPKGKAPLLIHTASLSQGVPSRFS 61
|||||

[illegible]

| Query Match | Best Local Similarity | Score | DB | Length |
|--|-----------------------|---------------------|-----------|---------|
| Matches 84; Conservative | 79.1%; | 424; | DB 4; | 107; |
| | 80.8%; | Pred. No. 4; 4e-40; | | |
| | 5; | Mismatches 15; | Indels 0; | Gaps 0; |
| | | | | |
| 2 MTGSPSSLSASVGRVTTTCRASQSIIRYLNMWYHKPKGAKPLIHTASSLSQGVSPRFS | 61 | | | |
| 4 MTGSPSSLSASVGRVTTTCRASQSIIRYLNMWYHKPKGAKPLIHTASSLSQGVSPRFS | 63 | | | |
| 62 GSAGTDPFTLTISLQPEDPATYTCQOSYTPPYFGGTGKQIK | 105 | | | |
| 64 GSAGTDPFTLTISLQPEDPATYTCQOSYTPPYFGGTGKQIK | 107 | | | |

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ID 09UL79 PRELIMINARY; PRT; 108 AA.
AC 09UL79;
DT 01-MAY-2000 (TEMBLrel. 13, Created)
DT 01-MAY-2000 (TEMBLrel. 13, Last sequence update)
DE 01-MAR-2003 (TEMBLrel. 23, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
   (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN 1
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
   fetus."
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035035; AAD56271.1; -.
DR HSSP; P01607; 1REI.
DR InterPro; IPR007110; Ig_1Ike.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG_LIKE; 1.
FT NON_TER 1
SQ SEQUENCE 108 AA; 11787 MW; DB5845F19724FBAE CRC64;

Query Match 77.5%; Score 421; DB 4; Length 108;
Best Local Similarity 79.0%; Pred. No. 1e-39;
Matches 83; Conservative 7; Mismatches 15; Indels 0; Gaps 0;

QY 1 VMTQSPSSLSASVGDRTVITCRASQSIIRYLMWYQHKPGAKPLIHHTASSLSQGVPSRF 60
DB 3 VMTQSPSSLSASVGDRTVITCRASQSIIRYLMWYQHKPGAKPLIHHTASSLSQGVPSRF 62
QY 61 GSVSGTDFLTITSSLOPEDPATYTCQOSTYTPYTCGQTKLQIK 105
DB 63 GSVSGTDFLTITSSLOPEDPATYTCQOSTYTPYTCGQTKLQIK 107

RESULT 6
Q96PF6 PRELIMINARY; PRT; 116 AA.
AC 096PF6;
DT 01-DEC-2001 (TEMBLrel. 19, Created)
DT 01-DEC-2001 (TEMBLrel. 19, Last sequence update)
DE 01-MAR-2003 (TEMBLrel. 23, Last annotation update)
DE Kappa 1 light chain variable region (Fragment).
GN SDNK1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN 1
RP SEQUENCE FROM N.A.
RX MEDLINE=21361171; PubMed=11468171;
RA Comenzo R.L., Zhang Y., Martinez C., Oseman K., Herrera G.A.;
RT "The triopism of organ involvement in primary systemic amyloidosis:
   contributions of Ig VL(D) germ line gene use and clonal plasma cell
   burden."
RL Blood 98:714-720(2001).
DR EMBL; AF361758; AAK51465.1; -.
DR InterPro; IPR007110; Ig_1Ike.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG_LIKE; 1.
FT NON_TER 1

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FT NON_TER 116
SQ SEQUENCE 116 AA; 12735 MW; E796FC2217BFCF57 CRC64;

Query Match 71.6%; Score 389; DB 4; Length 116;
Best Local Similarity 71.2%; Pred. No. 4.6e-36;
Matches 74; Conservative 11; Mismatches 19; Indels 0; Gaps 0;

QY 2 MTPQSPSSLSASVGDRTVITCRASQSIIRYLMWYQHKPGAKPLIHHTASSLSQGVPSRF 61
DB 4 MTPQSPSSLSASVGDRTVITCRASQSIIRYLMWYQHKPGAKPLIHHTASSLSQGVPSRF 63
QY 62 GSVSGTDFLTITSSLOPEDPATYTCQOSTYTPYTCGQTKLQIK 105
DB 64 GGSATNFTVTTITSSLOPEDPATYTCQOYHHLPTFTFGGQTKVDFK 107

RESULT 7
Q90YF0 PRELIMINARY; PRT; 298 AA.
AC 090YF0;
DT 01-MAY-2000 (TEMBLrel. 13, Created)
DT 01-MAY-2000 (TEMBLrel. 13, Last sequence update)
DE 01-MAR-2003 (TEMBLrel. 23, Last annotation update)
DE CN 8 scfv.
GN CN 8.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN 1
RP SEQUENCE FROM N.A.
RX STRAIN=Balb/c; TISSUE=Spleen;
RX MEDLINE=20183931; PubMed=10706631;
RA Shinohara N., Demura T., Fukuda H.;
RT "Isolation of a vascular cell wall-specific monoclonal antibody
   recognizing a cell polarity by using a phage display subtraction
   method."
RL Proc. Natl. Acad. Sci. U.S.A. 97:2585-2590(2000).
DR EMBL; AB036341; BAA88633.1; -.
DR HSSP; P01607; 1REI.
DR InterPro; IPR007110; Ig_1Ike.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00406; IGV; 2.
DR PROSITE; PSS0835; IG_LIKE; 2.
SQ SEQUENCE 298 AA; 31867 MW; E0F96B8A17004317 CRC64;

Query Match 69.6%; Score 378; DB 11; Length 298;
Best Local Similarity 68.3%; Pred. No. 2.6e-34;
Matches 71; Conservative 15; Mismatches 18; Indels 0; Gaps 0;

QY 2 MTPQSPSSLSASVGDRTVITCRASQSIIRYLMWYQHKPGAKPLIHHTASSLSQGVPSRF 61
DB 176 LTPQSPSSLSASVGEFTVITCRASQSIIRYLMWYQHKPGAKPLIHHTASSLSQGVPSRF 235
QY 62 GSVSGTDFLTITSSLOPEDPATYTCQOSTYTPYTCGQTKLQIK 105
DB 236 GGSATNFTVTTITSSLOPEDPATYTCQOYHHLPTFTFGGQTKLQIK 107

RESULT 8
Q920B6 PRELIMINARY; PRT; 109 AA.
AC 0920B6;
DT 01-DEC-2001 (TEMBLrel. 19, Created)
DT 01-DEC-2001 (TEMBLrel. 19, Last sequence update)
DE 01-MAR-2003 (TEMBLrel. 23, Last annotation update)
DE Pterin-mimicking anti-idiotope kappa chain variable region
   (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

```


| Db | Qy | Sequence | Score | Length | DB | Gap |
|-------------|--|--|----------------|-----------|-------------|-----|
| 2 | 1 | ITGSPASLSASVGEITVITTCRASINIVSYLAWYQKQKSGKSPQLLVYNAKTLADGVSRFS | 67.6% | 234 | 4 | 0 |
| Qy | 62 | GSVSGIDFTLTISLQPEDPATYTCQGSYTPPTFGSGTQIK 105 | | | | |
| Db | 84 | GSRGTFQSLKINSLOPEDGSGYCCQHSIGIPFTFGSTLEIK 127 | | | | |
| RESULT 12 | | | | | | |
| Q8NEK1 | ID | PRELIMINARY; | PRT; | 234 | AA. | |
| AC | Q8NEK1; | | | | | |
| DT | 01-OCT-2002 (TReMBLrel. 22, Created) | | | | | |
| DT | 01-OCT-2002 (TReMBLrel. 22, Last sequence update) | | | | | |
| DT | 01-MAR-2003 (TReMBLrel. 23, Last annotation update) | | | | | |
| DE | Hypothetical protein. | | | | | |
| OS | Homo sapiens (Human). | | | | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | | | |
| OC | Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. | | | | | |
| OX | NCBI_TaxID=9606; | | | | | |
| RN | [1] | | | | | |
| RP | SEQUENCE FROM N.A. | | | | | |
| RC | TISSUE=Lung; | | | | | |
| RL | Strasbourg R.; | | | | | |
| RL | Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases. | | | | | |
| DR | EMBL: BC030813; AAH30813.1; - | | | | | |
| DR | InterPro: IPR007110; Ig-like. | | | | | |
| DR | InterPro: IPR003597; Ig_cl. | | | | | |
| DR | InterPro: IPR003066; Ig_MHC. | | | | | |
| DR | InterPro: IPR003596; Ig_v. | | | | | |
| DR | Pfam: PF00047; Ig1; 2. | | | | | |
| DR | SMART: SM00407; IgC1; 1. | | | | | |
| DR | SMART: SM00406; IgV; 1. | | | | | |
| DR | PROSITE: PS50835; IG_LIKE; 2. | | | | | |
| DR | PROSITE: PS00290; IG_MHC; 1. | | | | | |
| DR | Hypothetical protein. | | | | | |
| SK | SEQUENCE 234 AA; 25530 MW; 6316E8DF8D132F8 CRC64; | | | | | |
| Query Match | | | | | | |
| | Best Local Similarity | 67.6%; | Score 367; | DB 4; | Length 234; | |
| | Matches 71; | Conservative 14; | Mismatches 20; | Indels 0; | Gaps | |
| Qy | 1 | VMTQSPSSLSASVDRITICRASQSIIRLNNYQHKGAPKLILHTASSLSQGVSPSR 60 | | | | |
| Db | 23 | VMTQSPATLSPSPERATLSCRASQSYTSLNLAWYQTFPGSPPLVLYGASSRRASGVPAR 82 | | | | |
| Qy | 61 | SGSVSGDFTLTISLQPEDPATYTCQGSYTPPTFGSGTQIK 105 | | | | |
| Db | 83 | SGSGSGTFEFTLTISLQSEDPATYTCQGNKMKPHTFQGTLDIK 127 | | | | |
| RESULT 13 | | | | | | |
| Q91WF8 | ID | PRELIMINARY; | PRT; | 234 | AA. | |
| AC | Q91WF8; | | | | | |
| DT | 01-DEC-2001 (TReMBLrel. 19, Created) | | | | | |
| DT | 01-DEC-2001 (TReMBLrel. 19, Last sequence update) | | | | | |
| DT | 01-MAR-2003 (TReMBLrel. 23, Last annotation update) | | | | | |
| DE | Hypothetical 25.9 kDa protein. | | | | | |
| OS | Mus musculus (Mouse). | | | | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | | | |
| OC | Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. | | | | | |
| OX | NCBI_TaxID=10090; | | | | | |
| RN | [1] | | | | | |
| RP | SEQUENCE FROM N.A. | | | | | |
| RC | TISSUE=Colon; | | | | | |
| RL | Strasbourg R.; | | | | | |
| RL | Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases. | | | | | |
| DR | EMBL: BC015292; AAH15292.1; - | | | | | |
| DR | InterPro: IPR003066; Ig_MHC. | | | | | |
| DR | InterPro: IPR003596; Ig_v. | | | | | |
| DR | InterPro: IPR001865; Ribosomal_S2. | | | | | |
| DR | Pfam: PF00047; Ig; 2. | | | | | |
| DR | SMART: SM00406; IgV; 1. | | | | | |

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DR PROSITE; PS00290; IG_MHC; 1.
DR PROSITE; PS00962; RIBOSOMAL_S2_1; 1.
KM Hypothetical protein.
SQ SEQUENCE 234 AA; 25929 MW; B0D0E6EB7812D2 CRC64;
Query Match
Best Local Similarity 67.6%; Score 367; DB 11; Length 234;
Matches 71; Conservative 12; Mismatches 21; Indels 0; Gaps 0;

QY 2 MTQSPSSLSASVGDRTVITCRASQSIIRILNYQHKFGKAPKLIHTTASSLSQGVPSRFS 61
DB MTQTSTSLASLGGRTVITCRASQDISNYLNWYQKQKPDGTVKLIITYTSRLYLGVPSRFS 83
QY 62 GSVAGTDFLTILISLQPEDPATYTCQOSYTPPYFGGCTLQIK 105
DB 84 GSGGTDYSLTISNLQEDIDATYFCQGGNPPTFGSGTLEVR 127

RESULT 14
Q920B9 PRELIMINARY; PRT; 111 AA.
ID Q920B9
AC Q920B9;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Plerin-mimicking anti-idiotope kappa chain variable region
(Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metacoa; Chordata; Cranialta; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Atkin J.D., Iape A., Jennings I.G., Horatis O., Cotton R.G.H.;
RT "Definition of the Idiotope of Plerin-Mimicking Antibodies Expressed
in Mamalian Cells."
RT Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
RL EMBL; AF307935; AL09419.1; -.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
PFam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG_LIKE; 1.
FT NON TER 1
FT NON TER 111
SQ SEQUENCE 111 AA; 12046 MW; 1E46988AA685826 CRC64;

Query Match
Best Local Similarity 66.3%; Score 360; DB 11; Length 111;
Matches 69; Conservative 17; Mismatches 19; Indels 4; Gaps 1;

QY 1 VMTQSPSSLSASVGDRTVITCRASQSI---IRILNMYQHKFGKAPKLIHTTASSLSQGV 56
DB 3 VLTQSPSSLSASVGDRTVITCRASQSVSTGYSTMYHQKPDGTVKLIITYLASNLSEGV 62
QY 57 PSRPSGVSAGNDFTLTISLQPEDPATYTCQOSYTPPYFGGCTLQIK 105
DB 63 PSRPSGVSAGNDFTLTISLQPEDPATYTCQOSYTPPYFGGCTLQIK 111

RESULT 15
Q9ERZ9 PRELIMINARY; PRT; 107 AA.
ID Q9ERZ9
AC Q9ERZ9;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Anti human TNF-alpha light chain variable region (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metacoa; Chordata; Cranialta; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;

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RN [1]
RP SEQUENCE FROM N.A.
RA Chen P., Deng J.B., Wang Z.L., Han H., Su C.Z.;
RT "Cloning and sequencing of the light chain fragment of variable region
RT genes of an anti-hTNF- $\alpha$  monoclonal antibody.";
RL J. Cell. Mol. Immunol. 12:21-26(1996).
RN [2]
RP SEQUENCE FROM N.A.
RA Chen P., Deng J.B., Wang Z.L., Han H., Yao L.B., Su C.Z.;
RT "Construction and sequencing of the single-chain antibody gene of a
RT human TNF- $\alpha$  specific monoclonal antibody.";
RL T1 4 Chun 1 Ta Hsueh Hsueh Pao 19:373-376(1998).
RN [3]
RP SEQUENCE FROM N.A.
RA Chen P., Deng J.B., Wang Z.L., Han H., Yao L.B., Su C.Z.;
RL Submitted (May-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF262753; AAG23804.1; -.
DR HSSP; P80362; 1WTL.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IgV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON TER 107
SQ SEQUENCE 107 AA; 11784 MW; 2B15EBA6604A26C3 CRC64;

Query Match 65.7%; Score 357; DB 11; Length 107;
Best Local Similarity 62.6%; Pred. No. 1,7e-32;
Matches 67; Conservative 18; Mismatches 16; Indels 6; Gaps 1;

QY 2 MTQSPSSLSASVGRVTITCRASQSI-----RYLNMYOHKPKGAPKLIHTASLSQSG 55
DB 1 MTQSPSSLSASVGRVTITCRASQSI-----RYLNMYOHKPKGAPKLIHTASLSQSG 55
QY 56 VPSRFGSGSVSGTDFLTITISLQPEDFATYYCOQSYTTPYTFGQGTKL 102
DB 61 VPDPRFMGSGSGTDFLTITISVQTEDLADYFCQCHYRTPTFTFGSGTKL 107

```

Search completed: January 22, 2004, 11:53:12
 Job time : 35 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 22, 2004, 11:37:35 ; Search time 32.8696 Seconds
(without alignments)
507.043 Million cell updates/sec

Title: US-09-147-443D-60
Perfect score: 543
Sequence: 1 VMTQSPSSLSASVGDRTIT.....CQSSYTPPYFGGQTKLQIK 105

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Listing first 45 summaries

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21: /SIDSI1/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:*

22: /SIDSI1/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*

23: /SIDSI1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*

24: /SIDSI1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----------|--------------------|
| 1 | 543 | 100.0 | 105 | AAW52241 | Antibody LDI/2-6-3 |
| 2 | 532 | 98.0 | 105 | AAW52243 | Antibody LDI/2-6-3 |
| 3 | 491 | 90.4 | 107 | AAW52260 | Anti-HIV gp120 imm |
| 4 | 491 | 90.4 | 107 | AAW01283 | VL region of HIV n |
| 5 | 491 | 90.4 | 107 | AAW55135 | Anti-gp120 antiod |
| 6 | 491 | 90.4 | 107 | AAW58244 | Anti-gp120 antiod |
| 7 | 488 | 89.9 | 111 | AAW63656 | Amino acid sequenc |
| 8 | 488 | 89.9 | 111 | ABJ38615 | Hepatitis C virus |
| 9 | 488 | 89.9 | 240 | ABJ38595 | Hepatitis C virus |

| | | | | | | |
|----|-------|------|-----|----|----------|--------------------|
| 10 | 488 | 89.9 | 299 | 22 | AAW63660 | Amino acid sequenc |
| 11 | 487 | 89.7 | 107 | 22 | AAW93593 | Human anti-Rh(D) a |
| 12 | 487 | 89.7 | 107 | 22 | AAW93544 | Human anti-Rh(D) a |
| 13 | 487 | 89.7 | 107 | 22 | AAW65567 | Amino acid sequenc |
| 14 | 487 | 89.7 | 114 | 22 | AAW65563 | Amino acid sequenc |
| 15 | 483 | 89.0 | 105 | 19 | AAW52217 | Antibody LDI-84-VL |
| 16 | 483 | 89.0 | 107 | 15 | AAW54261 | Anti-HIV gp120 imm |
| 17 | 483 | 89.0 | 107 | 17 | AAW01284 | VL region of HIV n |
| 18 | 483 | 89.0 | 107 | 21 | AAW95136 | Anti-gp120 antiod |
| 19 | 483 | 89.0 | 107 | 21 | AAW98245 | Anti-gp120 antiod |
| 20 | 483 | 89.0 | 132 | 18 | AAW28842 | Human anti-tumour |
| 21 | 482 | 88.8 | 107 | 22 | AAW93663 | Human anti-Rh(D) a |
| 22 | 482 | 88.8 | 107 | 22 | AAW93664 | Human anti-Rh(D) a |
| 23 | 482 | 88.8 | 108 | 24 | ABP96009 | HSA antibody relat |
| 24 | 482 | 88.8 | 114 | 18 | AAW13922 | light chain #1 for |
| 25 | 482 | 88.8 | 240 | 20 | AAW02472 | A single chain ant |
| 26 | 482 | 88.8 | 240 | 22 | AAW46005 | Human MUC-1 scfv c |
| 27 | 482 | 88.8 | 240 | 22 | AAW46006 | Human MUC-1 scfv c |
| 28 | 482 | 88.8 | 240 | 22 | AAW46007 | Human MUC-1 scfv c |
| 29 | 482 | 88.8 | 240 | 22 | AAW46008 | Human MUC-1 scfv c |
| 30 | 482 | 88.8 | 240 | 22 | AAW46038 | Human TF anti-ldio |
| 31 | 482 | 88.8 | 240 | 24 | ABP95997 | Human serum albumi |
| 32 | 481 | 88.6 | 107 | 22 | AAW93601 | Human anti-Rh(D) c |
| 33 | 480.5 | 88.5 | 108 | 22 | AAW93589 | Human anti-Rh(D) c |
| 34 | 480.5 | 88.5 | 108 | 22 | AAW93600 | Human anti-Rh(D) c |
| 35 | 480 | 88.4 | 107 | 18 | AAW16649 | Anti-cancer specif |
| 36 | 480 | 88.4 | 107 | 22 | AAW93594 | Human anti-Rh(D) c |
| 37 | 480 | 88.4 | 108 | 24 | AAW16706 | Human anti-blood c |
| 38 | 479 | 88.2 | 107 | 22 | AAW93667 | Human anti-Rh(D) a |
| 39 | 479 | 88.2 | 108 | 24 | AAW53210 | Human IGE scfv 1C2 |
| 40 | 477 | 87.8 | 104 | 15 | AAW54318 | Anti-HIV gp120 imm |
| 41 | 477 | 87.8 | 104 | 17 | AAW01285 | VL region of HIV n |
| 42 | 477 | 87.8 | 104 | 21 | AAW95137 | Anti-gp120 antiod |
| 43 | 477 | 87.8 | 104 | 21 | AAW98246 | Anti-gp120 antiod |
| 44 | 477 | 87.8 | 108 | 24 | AAW16708 | Human anti-blood c |
| 45 | 476.5 | 87.8 | 108 | 22 | AAW93655 | Human anti-Rh(D) a |

ALIGNMENTS

| | | |
|----------|---|----------------------------|
| RESULT 1 | AAW52241 | standard; protein; 105 AA. |
| ID | AAW52241 | |
| AC | AAW52241 | |
| XX | | |
| DT | 12-JUN-1998 | (first entry) |
| XX | | |
| DE | Antibody LDI/2-6-3-VL chain sequence. | |
| XX | | |
| KW | Antibody, variable heavy chain; VH chain; variable light chain; VL chain; | |
| KW | Rhesus D antigen; anti-Rhesus D immunoglobulin; HDN therapy; | |
| KW | idiopathic thrombocytopenic purpura; haemolytic disease of the newborn. | |
| OS | | |
| XX | Homo sapiens. | |
| XX | | |
| FN | WO9749809-A1. | |
| XX | | |
| PD | 31-DEC-1997. | |
| XX | | |
| PF | 20-JUN-1997. | 97WO-EP03253. |
| XX | | |
| FR | 24-JUN-1996. | 96EP-0810421. |
| XX | | |
| PA | (ROTK-) ROTKREUZSTIFTUNG ZENT LAB BLUTSPENDE. | |
| XX | | |
| PI | Amstutz H, Imboden M, Miescher S, Morell A, Stadler B; | |
| PI | Vogel M; | |
| DR | WPI; 1998-077173/07. | |
| DR | N-PDB; AAV19765. | |
| XX | | |

| | | |
|----|---|---------------|
| XX | 11-JUL-1995; | 95WO-US08743. |
| PF | | |
| XX | 18-JUL-1994; | 94US-0276852. |
| FR | | |
| XX | (SCRI) SCRIPPS RES INST. | |
| PA | | |
| XX | Barbas CF, Burton DR, Lerner RA; | |
| PI | | |
| XX | WPI; 1996-179601/18. | |
| DR | | |
| XX | | |
| PT | Monoclonal antibody binding to V1/V2 loop of HIV gp120 - used in | |
| PT | passive immuno:therapy and detection of HIV infection. | |
| XX | | |
| PS | Example; Fig 11, 366pp; English. | |
| XX | | |
| CC | The sequences given in AAW01261-92 represent the light chain variable | |
| CC | regions (VL) of a series of monoclonal antibodies (Mab's) which are | |
| CC | immunoreactive with HIV glycoprotein gp120 and are capable of | |
| CC | neutralising HIV. This sequence represents the sequence of the Jk2 | |
| CC | gene clones, b22 and B35. A Mab containing this VL sequence has the | |
| CC | capacity to reduce HIV infectivity titre in an in vivo virus | |
| CC | infectivity assay by 50 % at a concentration of less than 700 ng | |
| CC | of antibody/ml, and binds mature gp120 preferentially over the | |
| CC | precursor gp160. The Mab may be used for determining immunocompetence | |
| CC | of a human anti-HIV antibody and in the detection of HIV infection. | |
| XX | | |
| SQ | Sequence 107 AA; | |
| | | |
| | Query Match 90.4%; Score 491; DB 17; Length 107; | |
| | Best Local Similarity 91.3%; Pred. No. 3.5e-30; | |
| | Matches 99; Conservative 4; Mismatches 5; Indels 0; Gaps 0; | |
| QY | 2 MTGSPSSLSASVGDRTVTTCRASQSIIIRYLINWKYOKPKGKAPKLIIHTASSLQSGVPSRFS 61 | |
| Dd | 2 LTGSPSSLASAVDRAVTITCRASQSISSYLNWYQOKPKGKAPKLIIYAASSLQSGVPSRFS 61 | |
| QY | 62 GSVSQDPFTLTITSLQPEDPATYYCOOSYTTPYTFGGTQLQIK 105 | |
| Dd | 62 GSGSGDTFTLTITSLQPEDPATYYCOOSYSTPYTFGGTQLQIK 105 | |
| | | |
| | RESULT 5 | |
| | AAAY95135 | |
| ID | AAAY95135 standard; Protein; 107 AA. | |
| XX | | |
| AC | AAAY95135; | |
| XX | | |
| DT | 30-JUN-2000 (first entry) | |
| XX | | |
| DE | Anti-gp120 antibody light chain variable region from clone b22. | |
| XX | | |
| KM | Anti-human immunodeficiency virus type 1 antibody; HIV-1; neutralise; | |
| KW | reduce HIV infection; diagnosis; immuno:therapy; HIV induced disease; | |
| XX | glycoprotein 120; gp120; glycoprotein 41; gp41; monoclonal antibody. | |
| XX | | |
| OS | Homo sapiens. | |
| XX | | |
| PN | AU9948756-A. | |
| PD | 17-FEB-2000. | |
| XX | | |
| PP | 16-SEP-1999; 99AU-0048756. | |
| XX | | |
| PR | 16-SEP-1999; 99AU-0048756. | |
| XX | | |
| PA | (SCRI) SCRIPPS RES INST. | |
| XX | | |
| PI | Burton DR, Barbas CF, Lerner RA; | |
| XX | | |
| DR | WPI; 2000-293393/26. | |
| XX | | |
| TX | Novel human monoclonal antibodies which immunoreact with and neutralise | |

PT human immunodeficiency virus useful for treating HIV infections -
XX
PS Example 9; Figure 11; 366pp; English.
CC The present sequence represents a fragment of an anti-human
CC immunodeficiency virus type 1 (HIV-1) antibody. The invention relates to
CC a human whole immunoglobulin (Ig) molecule which immunoreacts with HIV
CC mature glycoprotein gp120 preferentially over HIV precursor glycoprotein
CC gp160 and neutralises HIV and which reduces HIV infectivity titre in an
CC in vitro virus infectivity assay by 50% at a concentration of less than
CC 700 ng/ml. The antibodies are used as reagents for the diagnosis and
CC immunotherapy of HIV induced disease. They are useful as neutralising
CC field isolates and provide useful information regarding the
CC immunocompetence of an immune response in HIV infected patients. The
CC monoclonal antibodies are useful for producing anti-idiotypic antibodies
CC which can be used to screen human monoclonal antibodies to identify
CC whether the antibody has the same binding specificity as the antibodies
CC of the invention. The neutralising antibodies define new epitopes on the
CC HIV gp120 and gp41 glycoproteins, thus increasing the availability of new
CC monoclonal antibodies for the treatment of HIV. A major advantage of the
CC monoclonal antibodies derives from the fact that they are encoded by a
CC human polynucleotide sequence. Thus in vivo use of the monoclonal
CC antibodies for diagnosis and immunotherapy of HIV induced disease greatly
CC reduces the problems of significant host immune response to the passively
CC administered antibodies which is a problem commonly encountered when
CC monoclonal antibodies of xenogeneic or chimeric derivation are utilized.
CC An additional major advantage of the monoclonal antibodies described
CC derives from the fact that they immunoreact with a unique determinant
CC present on mature HIV glycoprotein gp120. This class of antibodies is
CC particularly effective at neutralising field isolates of HIV.
XX
SQ Sequence 107 AA;
Query Match 90.4%; Score 491; DB 21; Length 107;
Best Local Similarity 91.3%; Pred. No. 3.5e-30;
Matches 95; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
QY 2 MTGSPSSLSASVGRVTTTCRASQSIIRYLNWYOHKPKGAKPLIHTASSLSQGVPSRFS 61
DB 2 LTQSPSSLSASVGRVTTTCRASQSIIRYLNWYOHKPKGAKPLIHTASSLSQGVPSRFS 61
62 GSVSCTDFTLTISLSQPEDFATYTCQOSYTPPTFGGTGLQIK 105
62 GSSGSDFTLTISLSQPEDFATYTCQOSYTPPTFGGTGLQIK 105
DB 62 GSSGSDFTLTISLSQPEDFATYTCQOSYTPPTFGGTGLQIK 105
QY 62 GSSGSDFTLTISLSQPEDFATYTCQOSYTPPTFGGTGLQIK 105
DB 62 GSSGSDFTLTISLSQPEDFATYTCQOSYTPPTFGGTGLQIK 105
RESULT 6
AA98244
ID AAY98244 standard; Protein; 107 AA.
XX
AC AAY98244;
XX
DT 04-JUL-2000 (first entry)
XX
DE Anti-gp120 antibody light chain variable region from clone b22.
XX
XX
KW Antibody; anti-HIV monoclonal antibody; glycoprotein-120;
KW human immunodeficiency virus type 1; HIV-1; infectivity titre;
KW passive immunotherapy; reduce severity; HIV-induced disease;
KW immunocompetence; active immunisation.
XX
OS Homo sapiens.
XX
FN AUY948754-A.
XX
PD 17-FEB-2000.
XX
XX 16-SEP-1999; 99AU-0048754.
XX
XX 16-SEP-1999; 99AU-0048754.
XX
PR 16-SEP-1999; 99AU-0048754.
XX
PA (SCRI) SCRIPPS RES INST.
XX

PI Burton DR, Barbas CF, Lerner RA;
XX
XX WPI; 2000-246867/22.
DR
XX
XX Human neutralising monoclonal antibodies to human immunodeficiency
PT virus (HIV) used for providing passive immunotherapy to HIV are
PT specific for glycoprotein-120 -
XX
PS Example 9; Figure 11; 374pp; English.
XX
XX This sequence represents a fragment of the antibodies of the invention.
CC The invention relates to the production of an anti-HIV (human
CC immunodeficiency virus) glycoprotein (gp)-120 monoclonal antibody
CC capable of reducing an HIV infectivity titre in an in vitro virus
CC infectivity assay by 50% at a concentration of less than 70 ng/ml. The
CC method for the production of the antibody comprises:
CC (a) providing a first polynucleotide encoding a heavy chain
CC immunoglobulin amino acid sequence (which does not comprise the sequence
CC represented by AAY98206) and a second polynucleotide encoding a light
CC chain immunoglobulin amino acid sequence;
CC (b) inserting the first and second polynucleotide sequences into a host
CC cell;
CC (c) maintaining the host cell in conditions which allow the amino acid
CC sequences encoded by the polynucleotides to be expressed in the host
CC cell; and
CC (d) isolating the antibody comprising the heavy and light chain
CC immunoglobulin amino acid sequences from the host cell.
CC The anti-HIV gp-120 monoclonal antibody is used for providing passive
CC immunotherapy to HIV in a human. They can be administered to high-risk
CC patients to reduce the likelihood and/or severity of HIV-induced disease
CC and to patients who are already HIV-infected. The antibodies are used
CC for neutralising field isolates which provides information about the
CC immunocompetence of an immune response in HIV patients, for detecting
CC HIV in a biological fluid or tissue sample e.g. by radioimmunoassay, for
CC producing anti-idiotypic antibodies which can be used for active
CC immunisation and to screen human monoclonal antibodies to identify those
CC with the same binding specificity and to monitor the course of HIV
CC disease therapy by measuring the changes in concentration of HIV present
CC in the body or in body fluids by immunoassay. The anti-HIV gp-120
CC monoclonal antibodies are encoded by a human polynucleotide sequence and
CC when used in vivo for diagnosis and immunotherapy of HIV-induced disease
CC reduce the problems of significant host immune response to the
CC antibodies associated with monoclonal antibodies of xenogeneic or
CC chimeric derivation.
XX
SQ Sequence 107 AA;
Query Match 90.4%; Score 491; DB 21; Length 107;
Best Local Similarity 91.3%; Pred. No. 3.5e-30;
Matches 95; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
QY 2 MTGSPSSLSASVGRVTTTCRASQSIIRYLNWYOHKPKGAKPLIHTASSLSQGVPSRFS 61
DB 2 LTQSPSSLSASVGRVTTTCRASQSIIRYLNWYOHKPKGAKPLIHTASSLSQGVPSRFS 61
62 GSVSCTDFTLTISLSQPEDFATYTCQOSYTPPTFGGTGLQIK 105
62 GSSGSDFTLTISLSQPEDFATYTCQOSYTPPTFGGTGLQIK 105
DB 62 GSSGSDFTLTISLSQPEDFATYTCQOSYTPPTFGGTGLQIK 105
QY 62 GSSGSDFTLTISLSQPEDFATYTCQOSYTPPTFGGTGLQIK 105
DB 62 GSSGSDFTLTISLSQPEDFATYTCQOSYTPPTFGGTGLQIK 105
RESULT 7
AAG63656
ID AAG63656 standard; Protein; 111 AA.
XX
AC AAG63656;
XX
DT 29-OCT-2001 (first entry)
XX
XX Amino acid sequence of the L chain variable region of ScFv3-4.
DE
XX
XX Complementarity determining region; CDR, single chain antibody; ScFv;
KW hepatitis C virus; HCV; HCV infection; CDR1; E2 protein; NS1 protein;
KW envelope glycoprotein.
XX

| | |
|-----------------------|--|
| XX | Homo sapiens. |
| XX | WO200158459-A1. |
| PN | 16-AUG-2001. |
| PD | 13-FEB-2001; 2001WO-JP00967. |
| PF | 14-FEB-2000; 2000JP-0034906. |
| PR | (MITS-) MITSUBISHI-TOKYO PHARM INC. |
| PA | Itami S, Shidui T, Seki M, Yotsumoto Y, Matsura Y, Miyamura T, |
| XX | WPI; 2001-496986/54. |
| DR | N-PSDB; AAH74685. |
| XX | Remedies for hepatitis C containing substances with antiviral effects |
| PT | e.g. antibodies, proteins, sulfated polysaccharides and low-molecular |
| PT | compounds, by inhibiting binding of hepatitis C virus envelope |
| PT | glycoprotein or CD81 - |
| XX | Claim 27; Page 116; 138pp; Japanese. |
| PS | The present sequence represents the L chain variable region of a single |
| CC | chain antibody of the invention. The specification describes a substance |
| CC | can inhibit the binding between hepatitis C virus (HCV) and cells with |
| CC | potential HCV infection, cells with expression of CD81, or CD81. This |
| CC | substance is especially an antibody with affinity towards HCV E2/NS1 |
| CC | protein, containing amino acid sequences based on the complementarity |
| CC | determining region (CDR 1, CDR2 and CDR3 of the H and L chain variable |
| CC | regions. The antibody inhibits the viral envelope glycoprotein. It is |
| CC | also a CDR1 inhibitor. The antibodies and drugs are used for treatment |
| CC | and/or prevention of hepatitis C, or for diagnosis of hepatitis C. |
| XX | |
| SQ | Sequence 111 AA; |
| Query Match | 89.9%; Score 488; DB 22; Length 111; |
| Best Local Similarity | 89.5%; Pred. No. 6.1e-30; |
| Matches | 94; Conservative 4; Mismatches 7; Indels 0; Gaps 0; |
| OY | 1 VMTGSPSSLSAVGDRTVITTCRASQSITIRYLNWYQHKGKAPKLIIHTASSLQGVPSRF 60 |
| Db | 3 VMTGSPSSLSAVGDRTVITTCRASQRISNYINWYQKPKAPKLIVYAASNLQGVPSRF 62 |
| OY | 61 SGVSVCSTFTLTSLQPEDPATFYCCOOSYTTPPYFGGTGLQIK 105 |
| Db | 63 SGSGSCTDFTLTSLQPEDPATFYCCOOSYTTPPYFGGTGLQIK 107 |
| RESULT 8 | |
| ID | ABJ38615 standard; Protein; 111 AA. |
| XX | ABJ38615; |
| AC | 12-JUN-2003 (first entry) |
| DT | Hepatitis C virus treatment related human protein sequence SEQ ID No 29. |
| DE | Vitruvian; inhibit; binding; hepatitis C virus; HCV; E2/NS1 protein; |
| XX | antibody; recombinant; antiviral; infection; human. |
| KW | Homo sapiens. |
| OS | WO2003014728-A1. |
| FN | 20-FEB-2003. |
| PD | 09-AUG-2002; 2002MO-JP08175. |
| XX | 10-AUG-2001; 2001JP-0243947. |
| FR | |

| | |
|-----------------------|---|
| XX | (MTS-) MITSUBISHI PHARMA CORP. |
| PA | (NINA-) JAPAN AGENCY NAT INST HEALTH. |
| PI | Itami S, Seki M, Kito M, Matsuura Y, Miyamura T; |
| PI | WPI, 2003-248334/24. |
| XX | |
| DR | |
| XX | Pharmaceutical compositions for hepatitis C containing screened |
| PT | inhibitors of binding between hepatitis virus (HCV) E2/NS1 protein and |
| PT | antibody, useful in preventing or treating HCV infections |
| XX | |
| PS | Example 4; Page 84; 136pp; Japanese. |
| XX | |
| CC | The invention relates to a novel method for screening substances |
| CC | inhibiting the binding of hepatitis C virus (HCV) E2/NS1 protein to an |
| CC | antibody having an affinity for the protein. The novel method comprises: |
| CC | contacting the protein with any of the antibodies selected, from those |
| CC | described in the specification, in the presence or absence of a test |
| CC | substance; and comparing the binding results. Compositions comprising the |
| CC | (recombinant) antibodies are useful as antivirals and are especially |
| CC | useful in preventing or treating HCV (hepatitis C) infections. This |
| CC | sequence represents a human protein relating to the novel HCV therapy |
| CC | method of the invention. |
| XX | |
| SO | Sequence 111 AA; |
| XX | |
| Query Match | 89.9%; Score 488; DB 24; Length 111; |
| Best Local Similarity | 89.5%; Pred. No. 6.1e-30; |
| Matches | 94; Conservative 4; Mismatches 7; Indels 0; Gaps 0; |
| QY | 1 VMTQSPSSLSASVGDRTVITCRASQSIIRYLNMYQHKPKGAPKLIHTASSLQSGVPSRF 60 |
| DB | 3 VMTQSPSSLSASVGDRTVITCRASQSIIRYLNMYQHKPKGAPKLIHTASSLQSGVPSRF 62 |
| QY | 61 SGASVSGTDFLTITSSLOPEDPATYCCQOSTPTPTFGCGKGLQIK 105 |
| DB | 63 SGSSGSGTDFLTITSSLOPEDPATYCCQOSTPTPTFGCGKGLQIK 107 |
| XX | |
| RESULT 9 | |
| ABJ38595 | |
| ID | ABJ38595 standard; Protein; 240 AA. |
| XX | |
| ABJ38595; | |
| XX | |
| DT | 12-JUN-2003 (first entry) |
| XX | |
| DE | Hepatitis C virus treatment related human protein sequence SEQ ID No 4. |
| XX | |
| KW | Vitruicide; inhibit; binding; hepatitis C virus; HCV; E2/NS1 protein; |
| XX | antibody; recombinant; antiviral; infection; human. |
| OS | Homo sapiens. |
| XX | |
| PN | WO2003014728-A1. |
| XX | |
| PD | 20-FEB-2003. |
| XX | |
| PF | 09-AUG-2002; 2002MO-JP08175. |
| XX | |
| PR | 10-AUG-2001; 2001JP-0243947. |
| XX | |
| PA | (MTS-) MITSUBISHI PHARMA CORP. |
| PA | (NINA-) JAPAN AGENCY NAT INST HEALTH. |
| XX | |
| P1 | Itami S, Seki M, Kito M, Matsuura Y, Miyamura T; |
| XX | |
| DR | WPI, 2003-248334/24. |
| XX | |
| PT | Pharmaceutical compositions for hepatitis C containing screened |
| PT | inhibitors of binding between hepatitis virus (HCV) E2/NS1 protein and |
| PT | antibody, useful in preventing or treating HCV infections |

XX Claim 1, Page 64-65; 136pp; Japanese.

CC The invention relates to a novel method for screening substances
 CC inhibiting the binding of hepatitis C virus (HCV) E2/NS1 protein to an
 CC antibody having an affinity for the protein. The novel method comprises:
 CC contacting the protein with any of the antibodies selected, from those
 CC described in the specification, in the presence or absence of a test
 CC substance, and comparing the binding results. Compositions comprising the
 CC (recombinant) antibodies are useful as antivirals and are especially
 CC useful in preventing or treating HCV (hepatitis C) infections. This
 CC sequence represents a human protein relating to the novel HCV therapy
 CC method of the invention.

XX Sequence 240 AA;

Query Match 89.9%; Score 488; DB 24; Length 240;
 Best Local Similarity 89.5%; Pred. No. 1.2e-29;
 Matches 94; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 1 VMTQSPSSLSASVGDRTITTCRASQSIIRYLNWYQHKGKAPKLLIHNTASSLSQGVPSRF 60
 DB 23 VMTQSPSSLSASVGDRTITTCRASQSIIRYLNWYQHKGKAPKLLIHNTASSLSQGVPSRF 82
 OY 61 SGSVSGTDFLTITSSLPEDPATYTCQOSYTTPTPGQGTKLQIK 105
 DB 83 SGSVSGTDFLTITSSLPEDPATYTCQOSYTTPTPGQGTKLQIK 127

RESULT 10
 AAG63660
 ID AAG63660 standard; Protein; 299 AA.

AC AAG63660;
 DT 29-OCT-2001 (first entry)

XX Amino acid sequence of single chain antibody ScFv3-4.

KM Complementarity determining region; CDR, single chain antibody; ScFv;
 KM hepatitis C virus; HCV; HCV infection; CD81; E2 protein; NS1 protein;
 KM envelope glycoprotein.

OS Homo sapiens.

XX MO200158459-A1.
 XX 16-AUG-2001.
 XX 13-FEB-2001; 2001WO-JP00967.
 XX 14-FEB-2000; 2000JP-0034906.
 XX (MITS-) MITSUBISHI-TOKYO PHARM INC.

XX Itami S, Shibui T, Seki M, Yotsunoto Y, Matsuura Y, Miyamura T;
 DR WPI; 2001-496986/54.
 DR N-PSDB; AAH74689.

XX Remedies for hepatitis C containing substances with antiviral effects
 PT e.g. antibodies, proteins, sulfated polysaccharides and low-molecular
 PT compounds, by inhibiting binding of hepatitis C virus envelope
 PT glycoprotein or CD81 -
 XX
 XX Disclosure; Page 127-129; 138pp; Japanese.

XX The present sequence represents a single chain antibody of the invention.
 CC The specification describes a substance can inhibit the binding between
 CC hepatitis C virus (HCV) and cells with potential HCV infection, cells
 CC with expression of CD81, or CD81. This substance is especially an
 CC antibody with affinity towards HCV E2/NS1 protein, containing amino acid
 NCC sequences based on the complementarity determining region (CDR) 1, CDR2

CC and CDR3 of the H and L chain variable regions. The antibody inhibits
 CC the viral envelope glycoprotein. It is also a CD81 inhibitor. The
 CC antibodies and drugs are used for treatment and/or prevention of
 CC hepatitis C, or for diagnosis of hepatitis C.

XX Sequence 299 AA;

Query Match 89.9%; Score 488; DB 22; Length 299;
 Best Local Similarity 89.5%; Pred. No. 1.5e-29;
 Matches 94; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 1 VMTQSPSSLSASVGDRTITTCRASQSIIRYLNWYQHKGKAPKLLIHNTASSLSQGVPSRF 60
 DB 168 VMTQSPSSLSASVGDRTITTCRASQSIIRYLNWYQHKGKAPKLLIHNTASSLSQGVPSRF 227
 OY 61 SGSVSGTDFLTITSSLPEDPATYTCQOSYTTPTPGQGTKLQIK 105
 DB 228 SGSVSGTDFLTITSSLPEDPATYTCQOSYTTPTPGQGTKLQIK 272

RESULT 11
 AAG93593
 ID AAG93593 standard; Protein; 107 AA.

AC AAG93593;
 DT 14-SEP-2001 (first entry)

XX Human anti-Rh(D) chain 105 protein sequence.

XX Human; anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;
 KM red blood cell; Rh phenotype; diagnosis; therapeutic.

OS Homo sapiens.

XX US6255455-B1.
 XX 03-JUL-2001.
 XX 29-JAN-1999; 99US-0240274.
 XX 11-OCT-1996; 96US-0028550.
 XX 10-APR-1998; 98US-0081380.
 XX 27-JUN-1997; 97US-0884045.

XX (UYPE-) UNIV PENNSYLVANIA.
 XX Siegel DL;
 XX WPI; 2001-388931/41.
 XX N-PSDB; AAH68650.

XX New isolated protein, preferably a human anti-Rh(D) antibody for use in
 PT diagnostics requiring a human instead of an animal antibody and in
 PT therapeutic medicine -
 XX
 XX Claim 1; Column 44; 162pp; English.

XX The present invention describes an isolated Rh(D) binding protein.
 CC preferably a human antibody, (1) having an amino acid sequence comprising
 CC one of the sequences (S) given in AAG93558 to AAG93659. (1) has
 CC immunostimulant activity, and can be used as an immune system stimulant.
 CC (1) can be used in diagnostic and therapeutic medicine. The antibodies
 CC are used in diagnostics that require human antibodies instead of animal
 CC antibodies, such as determine the Rh phenotype of human red blood cells.
 CC AAH68615 to AAH68726 represent the nucleotide sequence which encode
 CC AAG93558 to AAG93659. AAG93670 to AAG93697 represent anti-Rh(D) heavy
 CC chain CDR3 amino acid sequences which are given in the exemplification
 CC of the present invention.

XX Sequence 107 AA;
 Query Match 89.7%; Score 487; DB 22; Length 107;

Best Local Similarity 90.4%; Pred. No. 7e-30;
Matches 94; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 2 MTQSPSSLSASVGRVITTCRASQSIIRYLNWYOHKPKKPLIHTASSLSQGVPSRF 61
DB 3 LTQSPSSLSASVGRVITTCRASQSIIRYLNWYOHKPKKPLIHTASSLSQGVPSRF 62
QY 62 GSVSGTDFLTITISLQPEDFATYCCQSYTTPYFGQGTQLQIK 105
DB 63 GSGSGTDFLTITISLQPEDFATYCCQSYTTPYFGQGTQLQIK 106

RESULT 12

AAAG3644
ID AAG3644 standard; Protein; 107 AA.
XX
XX AAG3644;
AC
XX 14-SBP-2001 (first entry)
XX
XX Human anti-Rh(D) antibody clone SH13 protein sequence.
DE
XX Human; anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;
KW red blood cell; Rh phenotype; diagnosis; therapeutic.
XX
XX Homo sapiens.
XX
XX US6255455-B1.
XX
XX 03-JUL-2001.
XX
XX 29-JAN-1999; 99US-0240274.
XX
XX 11-OCT-1996; 96US-0028550.
PR 10-APR-1998; 98US-0081380.
PR 27-JUN-1997; 97US-0884045.
XX
XX (UYPE-) UNIV PENNSYLVANIA.
XX
XX
PI Siegel DL;
XX
XX WPI; 2001-388931/41.
DR N-PSDB; AAH68701.
XX
XX PT New isolated protein, preferably a human anti-Rh(D) antibody for use in
PT diagnostics requiring a human instead of an animal antibody and in
PT therapeutic medicine.
XX
XX
PS Claim 1; Column 68; 162pp; English.
XX
XX The present invention describes an isolated Rh(D) binding protein,
CC preferably a human antibody, (I) having an amino acid sequence comprising
CC one of the sequences (S) given in AAG3658 to AAG3669. (I) has
CC immunostimulant activity, and can be used as an immune system stimulant.
CC (I) can be used in diagnostic and therapeutic medicine. The antibodies
CC are used in diagnostics that require human antibodies instead of animal
CC antibodies, such as determine the Rh phenotype of human red blood cells.
CC AAH68615 to AAH68726 represent the nucleotide sequence which encode
CC AAG3658 to AAG3669. AAG3670 to AAG3697 represent anti-Rh(D) heavy
CC chain CDR3 amino acid sequences which are given in the exemplification
CC of the present invention.
XX
XX
SQ Sequence 107 AA;

Query Match 89.7%; Score 487; DB 22; Length 107;
Best Local Similarity 90.4%; Pred. No. 7e-30;
Matches 94; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 2 MTQSPSSLSASVGRVITTCRASQSIIRYLNWYOHKPKKPLIHTASSLSQGVPSRF 61
DB 3 LTQSPSSLSASVGRVITTCRASQSIIRYLNWYOHKPKKPLIHTASSLSQGVPSRF 62
QY 62 GSVSGTDFLTITISLQPEDFATYCCQSYTTPYFGQGTQLQIK 105

DB 63 GSGSGTDFLTITISLQPEDFATYCCQSYTTPYFGQGTQLQIK 106

RESULT 13

AAAG5567
ID AAG5567 standard; protein; 107 AA.
XX
XX AAG5567;
AC
XX 30-NOV-2001 (first entry)
DT
XX Amino acid sequence of protein seq Id No. 92.
DE
XX Gene library; immunoglobulin; antibody library; human.
KM
XX Homo sapiens.
OS
XX WO200162907-A1.
PN
XX 30-AUG-2001.
PD
XX
PF 22-FEB-2001; 2001WO-IP01298.
XX
XX 22-FEB-2000; 2000JP-0050543.
PR
XX (MED-) MEDICAL & BIOLOGICAL LAB CO LTD.
PA
XX Kurosawa Y, Akahori Y, Iba Y, Morino K, Shinohara M, Takahashi M;
XX Okuno Y, Shiraki K;
PI
XX WPI; 2001-565420/63.
DR N-PSDB; AAH47731.
XX
XX Producing gene libraries and antibody libraries, involves selecting a
PT light chain that binds to a heavy chain product to produce a functional
PT formation, and producing a gene library of the light chain variable
PT regions -
XX
XX
PS Examples; p 167-168; 181pp; Japanese.
XX
XX The invention relates to producing gene libraries, comprising
CC immunoglobulin light and heavy variable region. The method involves
CC selecting light chain that binds with the heavy chain product to produce
CC a functional conformation, producing a gene library comprising a
CC collection of these light chain variable genes, and combining with gene
CC library of heavy chain variable genes. The method is used for production
CC of gene and antibody libraries.
XX
XX
SQ Sequence 107 AA;

Query Match 89.7%; Score 487; DB 22; Length 107;
Best Local Similarity 90.5%; Pred. No. 7e-30;
Matches 95; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 WMTQSPSSLSASVGRVITTCRASQSIIRYLNWYOHKPKKPLIHTASSLSQGVPSRF 60
DB 3 WMTQSPSSLSASVGRVITTCRASQSIIRYLNWYOHKPKKPLIHTASSLSQGVPSRF 62
QY 61 GSVSGTDFLTITISLQPEDFATYCCQSYTTPYFGQGTQLQIK 105
DB 63 GSGSGTDFLTITISLQPEDFATYCCQSYTTPYFGQGTQLQIK 107

RESULT 14

AAAG5563
ID AAG5563 standard; protein; 114 AA.
XX
XX AAG5563;
AC
XX 30-NOV-2001 (first entry)
DT
XX Amino acid sequence of protein seq Id No. 88.

XX Gene library; immunoglobulin; antibody library; human.
 XX Homo sapiens.
 XX WO200162907-A1.
 XX 30-AUG-2001.
 XX 22-FEB-2001; 2001WO-JP01298.
 XX 22-FEB-2000; 2000JP-0050543.
 XX (MEDI-) MEDICAL & BIOLOGICAL LAB CO LTD.
 XX Kurosawa Y, Akahori Y, Iba Y, Morino K, Shinohara M, Takahashi M,
 XX Okuno Y, Shiraki K;
 XX WPI; 2001-565420/63.
 XX N-PSDB; AAH47727.
 XX Producing gene libraries and antibody libraries, involves selecting a
 XX light chain that binds to a heavy chain product to produce a functional
 XX formation, and producing a gene library of the light chain variable
 XX regions -
 XX Examples; p 162-163; 181pp; Japanese.
 XX The invention relates to producing gene libraries, comprising
 XX immunoglobulin light and heavy variable region. The method involves
 XX selecting light chain that binds with the heavy chain product to produce
 XX a functional conformation, producing a gene library comprising a
 XX collection of these light chain variable genes, and combining with gene
 XX library of heavy chain variable genes. The method is used for production
 XX of gene and antibody libraries.
 XX Sequence 114 AA;

Query Match 89.7%; Score 487; DB 22; Length 114;
 Best Local Similarity 90.5%; Pred. No. 7.4e-30;
 Matches 95; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
 QY 1 VMTQSPSSLSASVGRVTITCRASQSIIRYLNMYQHKGKAPKLLIHTASSLSQGVPSRF 60
 DB 3 VMTQSPSSLSASVGRVTITCRASQSIIRYLNMYQHKGKAPKLLIHTASSLSQGVPSRF 62
 QY 61 SSVSVSGTDFLTITSLQPEDFATYYCOQSYTTPYTFGGTKLQIK 105
 DB 63 SSVSVSGTDFLTITSLQPEDFATYYCOQSYTTPYTFGGTKLQIK 107

RESULT 15
 AAW52217
 ID AAW52217 standard; Protein; 105 AA.
 XX AAW52217;
 XX AAW52217;
 XX 12-JUN-1998 (first entry)
 XX Antibody LD1-84-VL chain sequence.
 XX Antibody; variable heavy chain; VH chain; variable light chain; VL chain;
 XX Rhesus D antigen; anti-Rhesus D immunoglobulin; HDN; therapy;
 XX idiopathic thrombocytopenic purpura; haemolytic disease of the newborn.
 XX Homo sapiens.
 XX WO9749809-A1.
 XX 31-DEC-1997.
 XX 20-JUN-1997; 97WO-EP03253.

PR 24-JUN-1996; 96EP-0810421.
 XX (ROTK-) ROTKREUTZSTIFTUNG ZENT LAB BLUTSPENDE.
 XX Amstutz H, Imboden M, Miescher S, Morell A, Stadler B;
 XX Vogel M;
 XX WPI; 1998-077173/07.
 XX N-PSDB; AAV19741.
 XX New Rhesus D antigen binding polypeptide(s) - used to neutralise
 XX Rhesus D antigen in therapy, e.g. for treating idiopathic
 XX thrombocytopenic purpura
 XX Claim 1; Fig 3B; 68pp; English.
 XX This sequence is the antibody LD1-84-VL chain sequence, which is a
 XX polypeptide of the invention. The polypeptides are capable of forming
 XX antigen binding structures with specificity for Rhesus D antigens which
 XX include Rhesus D-specific CDR 1, CDR 2, and CDR 3 regions of pairs of
 XX variable heavy (VH) and variable light (VL) chain sequences. The
 XX antibodies are active against the Rhesus D antigen. They can be used for
 XX treating disorders which would benefit from anti-Rhesus D immunoglobulin,
 XX e.g. idiopathic thrombocytopenic purpura. They can also be used for the
 XX protection of Rhesus negative women before or immediately after the birth
 XX of a Rhesus positive child to prevent haemolytic disease of the newborn
 XX (HDN) in subsequent pregnancies. In addition, anti-Rhesus D
 XX immunoglobulin can be used after transfusions of Rhesus positive blood
 XX to Rhesus negative recipients in order to prevent sensitisation to the
 XX Rhesus D antigen. The products can also be used as diagnostic reagents.
 XX Sequence 105 AA;

Query Match 89.0%; Score 483; DB 19; Length 105;
 Best Local Similarity 87.6%; Pred. No. 1.4e-29;
 Matches 92; Conservative 6; Mismatches 7; Indels 0; Gaps 0;
 QY 1 VMTQSPSSLSASVGRVTITCRASQSIIRYLNMYQHKGKAPKLLIHTASSLSQGVPSRF 60
 DB 1 VMTQSPSSLSASVGRVTITCRASQSIIRYLNMYQHKGKAPKLLIHTASSLSQGVPSRF 60
 QY 61 SSVSVSGTDFLTITSLQPEDFATYYCOQSYTTPYTFGGTKLQIK 105
 DB 61 SSVSVSGTDFLTITSLQPEDFATYYCOQSYRBFETGRGTSIDIK 105

Search completed: January 22, 2004, 11:51:22
 Job time : 34.8696 secs

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OM protein - protein search, using sw model

Run on: January 22, 2004, 11:53:16 ; Search time 31.5 Seconds
(without alignments)
689.122 Million cell updates/sec

Title: US-09-147-443D-60
Perfect score: 543
Sequence: 1 VMTQSPSSISASVGRVTIT.....CQGSYTPYFGQGTMLQIK 105

Scoring table: BLOSUM62
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Maximum Match 100%
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Database :

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2: /cgn2_6/ptodata/1/pubppa/PC7_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubppa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubppa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubppa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubppa/PC7US_PUBCOMB.pep:*
7: /cgn2_6/ptodata/1/pubppa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubppa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/1/pubppa/US09_PUBCOMB.pep:*
10: /cgn2_6/ptodata/1/pubppa/US09_PUBCOMB.pep:*
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14: /cgn2_6/ptodata/1/pubppa/US10_PUBCOMB.pep:*
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18: /cgn2_6/ptodata/1/pubppa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------------|
| 1 | 491 | 90.4 | 107 | 12 | US-10-016-986-104 |
| 2 | 488 | 89.9 | 111 | 12 | US-10-203-754A-57 |
| 3 | 487 | 89.7 | 107 | 11 | US-09-848-798-36 |
| 4 | 486 | 89.7 | 107 | 11 | US-09-848-798-156 |
| 5 | 485 | 89.5 | 107 | 11 | US-09-791-153A-67 |
| 6 | 483 | 89.0 | 107 | 12 | US-10-016-986-105 |
| 7 | 482 | 88.8 | 107 | 11 | US-09-848-798-175 |
| 8 | 482 | 88.8 | 107 | 11 | US-09-848-798-176 |
| 9 | 482 | 88.8 | 240 | 9 | US-09-192-854-2 |
| 10 | 482 | 88.8 | 240 | 10 | US-09-968-561A-2 |
| 11 | 482 | 88.8 | 240 | 12 | US-09-968-744A-2 |
| 12 | 481 | 88.6 | 107 | 11 | US-09-848-798-44 |
| 13 | 480.5 | 88.5 | 108 | 11 | US-09-848-798-32 |
| 14 | 480.5 | 88.5 | 108 | 11 | US-09-848-798-43 |
| 15 | 480 | 88.4 | 107 | 11 | US-09-848-798-37 |

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| 16 | 479 | 88.2 | 107 | 11 | US-09-848-798-179 | Sequence 179, App |
| 17 | 477 | 87.8 | 104 | 12 | US-10-016-986-106 | Sequence 106, App |
| 18 | 476.5 | 87.8 | 108 | 11 | US-09-848-798-167 | Sequence 167, App |
| 19 | 476 | 87.7 | 111 | 12 | US-10-203-754A-56 | Sequence 56, Appl |
| 20 | 474 | 87.3 | 107 | 12 | US-10-016-986-103 | Sequence 103, Appl |
| 21 | 473 | 87.1 | 107 | 11 | US-09-848-798-33 | Sequence 33, Appl |
| 22 | 472 | 86.9 | 107 | 11 | US-09-848-798-38 | Sequence 38, Appl |
| 23 | 472 | 86.9 | 107 | 11 | US-09-848-798-39 | Sequence 39, Appl |
| 24 | 471 | 86.7 | 106 | 12 | US-10-377-121-5 | Sequence 5, Appl |
| 25 | 471 | 86.7 | 107 | 11 | US-09-848-798-158 | Sequence 158, App |
| 26 | 469 | 86.4 | 214 | 15 | US-10-153-382-19 | Sequence 19, Appl |
| 27 | 468 | 86.2 | 108 | 14 | US-10-025-687-8 | Sequence 8, Appl |
| 28 | 468 | 86.2 | 108 | 15 | US-10-125-687-8 | Sequence 8, Appl |
| 29 | 466.5 | 85.8 | 108 | 11 | US-09-848-798-181 | Sequence 181, App |
| 30 | 466 | 85.8 | 107 | 11 | US-09-848-798-35 | Sequence 35, Appl |
| 31 | 465 | 85.6 | 107 | 11 | US-09-848-798-173 | Sequence 173, App |
| 32 | 465 | 85.6 | 109 | 12 | US-10-330-613-10 | Sequence 10, Appl |
| 33 | 465 | 85.6 | 109 | 12 | US-10-330-530-10 | Sequence 10, Appl |
| 34 | 463.5 | 85.4 | 108 | 11 | US-09-848-798-41 | Sequence 41, Appl |
| 35 | 463.5 | 85.4 | 250 | 11 | US-09-880-748-1174 | Sequence 1174, Ap |
| 36 | 463 | 85.3 | 127 | 15 | US-10-283-349-71 | Sequence 71, Appl |
| 37 | 462 | 85.1 | 107 | 11 | US-09-848-798-168 | Sequence 168, App |
| 38 | 461.5 | 85.0 | 108 | 11 | US-09-848-798-163 | Sequence 163, App |
| 39 | 461 | 84.9 | 106 | 8 | US-08-844-215-13 | Sequence 13, Appl |
| 40 | 461 | 84.9 | 107 | 11 | US-09-848-798-40 | Sequence 40, Appl |
| 41 | 460 | 84.7 | 237 | 11 | US-09-880-748-1906 | Sequence 1906, Ap |
| 42 | 460 | 84.7 | 237 | 11 | US-09-880-748-2003 | Sequence 2003, Ap |
| 43 | 460 | 84.7 | 237 | 11 | US-09-880-748-2005 | Sequence 2005, Ap |
| 44 | 460 | 84.7 | 237 | 11 | US-09-880-748-2017 | Sequence 2017, Ap |
| 45 | 460 | 84.7 | 237 | 11 | US-09-880-748-2019 | Sequence 2019, Ap |

ALIGNMENTS

RESULT 1
US-10-016-986-104
; Sequence 104, Application US/10016986
; Publication No. US20030187247A1
; GENERAL INFORMATION:
; APPLICANT: Burton, Dennis R.
; APPLICANT: Barbas, Carlos F.
; TITLE OF INVENTION: Lerner, Richard A.
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; FILE REFERENCE: 313.2CON1
; CURRENT APPLICATION NUMBER: US/10/016,986
; CURRENT FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: US 09/149,898
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: US 08/899,575
; PRIOR FILING DATE: 1997-07-24
; PRIOR APPLICATION NUMBER: US 08/276,852
; PRIOR FILING DATE: 1994-07-18
; PRIOR APPLICATION NUMBER: US 08/178,302
; PRIOR FILING DATE: 1994-01-06
; PRIOR APPLICATION NUMBER: PCT/US93/09328
; PRIOR FILING DATE: 1993-09-30
; PRIOR APPLICATION NUMBER: US 07/954,148
; PRIOR FILING DATE: 1992-09-30
; NUMBER OF SEQ ID NOS: 176
; SOFTWARE: FaastSeq for Windows Version 4.0
; SEQ ID NO 104
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthesized
US-10-016-986-104

Query Match 90.4%; Score 491; DB 12; Length 107;
Best Local Similarity 91.3%; Pred. No. 7.2e-38;
Matches 95; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Query Match 89.5%; Score 486; DB 11; Length 107;
Best Local Similarity 90.4%; Pred. No. 2.1e-37;
Matches 94; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 2 MTQSPSSLSASVGDRTVITCRASQSIIRYLNWYQHKRGKAPKLLIHTASSLQSGVPSRFS 61
DB 4 MTQSPSSLSASVGDRTVITCRASQSIIRYLNWYQHKRGKAPKLLIHTASSLQSGVPSRFS 63

QY 62 GSVSGTDFLTITISLQPEDFATYCCQSYTPTPTFGQGTLOIK 105
DB 64 GSGSGTDFLTITISLQPEDFATYCCQSYTPTPTFGQGTLOIK 107

RESULT 6
US-10-016-986-105
Sequence 105, Application US/10016986
Publication No. US20030187247A1
GENERAL INFORMATION:
APPLICANT: Burton, Dennis R
APPLICANT: Barbas, Carlos F
APPLICANT: Lerner, Richard A
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
FILE REFERENCE: 313.2CON1
CURRENT APPLICATION NUMBER: US/10/016,986
PRIOR FILING DATE: 2001-12-12
PRIOR APPLICATION NUMBER: US 09/149,898
PRIOR FILING DATE: 1998-09-08
PRIOR APPLICATION NUMBER: US 08/899,575
PRIOR FILING DATE: 1997-07-24
PRIOR APPLICATION NUMBER: US 08/276,852
PRIOR FILING DATE: 1994-07-18
PRIOR APPLICATION NUMBER: US 08/178,302
PRIOR FILING DATE: 1994-01-06
PRIOR APPLICATION NUMBER: PCT/US93/09328
PRIOR FILING DATE: 1993-09-30
PRIOR APPLICATION NUMBER: US 07/954,148
PRIOR FILING DATE: 1992-09-30
NUMBER OF SEQ ID NOS: 176
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 105
LENGTH: 107
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthesized
US-10-016-986-105.

Query Match 89.0%; Score 483; DB 12; Length 107;
Best Local Similarity 90.4%; Pred. No. 3.9e-37;
Matches 94; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 2 MTQSPSSLSASVGDRTVITCRASQSIIRYLNWYQHKRGKAPKLLIHTASSLQSGVPSRFS 61
DB 2 LTQSPSSLSASVGDRTVITCRASQSIIRYLNWYQHKRGKAPKLLIHTASSLQSGVPSRFS 61

QY 62 GSVSGTDFLTITISLQPEDFATYCCQSYTPTPTFGQGTLOIK 105
DB 62 GSGSGTDFLTITISLQPEDFATYCCQSYTPTPTFGQGTLOIK 105

RESULT 7
US-09-848-798-175
Sequence 175, Application US/09848798
Publication No. US20030040605A1
GENERAL INFORMATION:
APPLICANT: Siegel, Donald L
TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
FILE REFERENCE: 09596-4202
CURRENT APPLICATION NUMBER: US/09/848,798
CURRENT FILING DATE: 2001-05-04

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 175
LENGTH: 107
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: anti-Rh(D) antibody clone SH49
US-09-848-798-175

Query Match 88.8%; Score 482; DB 11; Length 107;
Best Local Similarity 88.5%; Pred. No. 4.8e-37;
Matches 92; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 2 MTQSPSSLSASVGDRTVITCRASQSIIRYLNWYQHKRGKAPKLLIHTASSLQSGVPSRFS 61
DB 3 LTQSPSSLSASVGDRTVITCRASQSIIRYLNWYQHKRGKAPKLLIHTASSLQSGVPSRFS 62

QY 62 GSVSGTDFLTITISLQPEDFATYCCQSYTPTPTFGQGTLOIK 105
DB 63 GSGSGTDFLTITISLQPEDFATYCCQSYTPTPTFGQGTLOIK 106

RESULT 8
US-09-848-798-176
Sequence 176, Application US/09848798
Publication No. US20030040605A1
GENERAL INFORMATION:
APPLICANT: Siegel, Donald L
TITLE OF INVENTION: SORTING PROTEINS AND MAGNETICALLY ACTIVATED CELL
FILE REFERENCE: 09596-4202
CURRENT APPLICATION NUMBER: US/09/848,798
PRIOR FILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 176
LENGTH: 107
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: anti-Rh(D) antibody clone SH50
US-09-848-798-176

Query Match 88.8%; Score 482; DB 11; Length 107;
Best Local Similarity 88.5%; Pred. No. 4.8e-37;
Matches 92; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 2 MTQSPSSLSASVGDRTVITCRASQSIIRYLNWYQHKRGKAPKLLIHTASSLQSGVPSRFS 61
DB 3 LTQSPSSLSASVGDRTVITCRASQSIIRYLNWYQHKRGKAPKLLIHTASSLQSGVPSRFS 62

QY 62 GSVSGTDFLTITISLQPEDFATYCCQSYTPTPTFGQGTLOIK 105
DB 63 GSGSGTDFLTITISLQPEDFATYCCQSYTPTPTFGQGTLOIK 106

RESULT 9
US-09-192-854-2
Sequence 2, Application US/09192854
Patent No. US20020068276A1
GENERAL INFORMATION:
APPLICANT: Winter, Greg
APPLICANT: Tomlinson, Ian
TITLE OF INVENTION: Methods for Selecting Functional Peptides

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FILE REFERENCE: 3789/72916
CURRENT APPLICATION NUMBER: US/09/192,854
CURRENT FILING DATE: 1998-11-17
EARLIER APPLICATION NUMBER: 60/066,729
EARLIER FILING DATE: 1997-11-21
NUMBER OF SEQ ID NOS: 212
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 240
TYPE: PRT
ORGANISM: Homo sapiens
US-09-192-854-2

Query Match      88.8%; Score 482; DB 9; Length 240;
Best Local Similarity 90.4%; Pred. No. 1,1e-36;
Matches 94; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 2 MTQSPSSLSASVGDVAVTTTCRASQSIIRYLNWYQHKRGPAPKLLIHTASSLSQGVSPSRFS 61
DB 136 MTQSPSSLSASVGDVAVTTTCRASQSIIRYLNWYQHKRGPAPKLLIHTASSLSQGVSPSRFS 195

QY 62 GSVSGTDFLTITSSLSQPEDFATYYCQOSYTTPTFGGQTKLQIK 105
DB 196 GSVSGTDFLTITSSLSQPEDFATYYCQOSYTTPTFGGQTKVEIK 239

RESULT 10
US-09-968-561A-2
Sequence 2, Application US/09968561A
Patent No. US2002016462A1
GENERAL INFORMATION:
APPLICANT: Tomlinson, Ian M
APPLICANT: Winter, Gregory
TITLE OF INVENTION: Method to Screen Phage Display Libraries with Different Ligands
FILE REFERENCE: 8039/1073B
CURRENT APPLICATION NUMBER: US/09/968,561A
CURRENT FILING DATE: 2001-10-01
PRIOR APPLICATION NUMBER: GB 9722131.1
PRIOR FILING DATE: 1997-10-20
PRIOR APPLICATION NUMBER: US 60/065,248
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: US 60/066,729
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: PCT/GB98/03135
PRIOR FILING DATE: 1998-10-20
PRIOR APPLICATION NUMBER: US 09/511,939
PRIOR FILING DATE: 2000-02-24
NUMBER OF SEQ ID NOS: 350
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 240
TYPE: PRT
ORGANISM: Homo sapiens
US-09-968-561A-2

Query Match      88.8%; Score 482; DB 10; Length 240;
Best Local Similarity 90.4%; Pred. No. 1,1e-36;
Matches 94; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 2 MTQSPSSLSASVGDVAVTTTCRASQSIIRYLNWYQHKRGPAPKLLIHTASSLSQGVSPSRFS 61
DB 136 MTQSPSSLSASVGDVAVTTTCRASQSIIRYLNWYQHKRGPAPKLLIHTASSLSQGVSPSRFS 195

QY 62 GSVSGTDFLTITSSLSQPEDFATYYCQOSYTTPTFGGQTKLQIK 105
DB 196 GSVSGTDFLTITSSLSQPEDFATYYCQOSYTTPTFGGQTKVEIK 239

RESULT 11
US-09-968-744A-2
Sequence 2, Application US/09968744A
Publication No. US20030148372A1
GENERAL INFORMATION:
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APPLICANT: Tomlinson, Ian M
APPLICANT: Winter, Gregory
TITLE OF INVENTION: Method to Screen Phage Display Libraries with Different Ligands
FILE REFERENCE: 8039/1073
CURRENT APPLICATION NUMBER: US/09/968,744A
CURRENT FILING DATE: 2003-01-13
PRIOR APPLICATION NUMBER: GB 9722131.1
PRIOR FILING DATE: 1997-10-20
PRIOR APPLICATION NUMBER: US 60/065,248
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: US 60/066,729
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: PCT/GB98/03135
PRIOR FILING DATE: 1998-10-20
PRIOR APPLICATION NUMBER: US 09/511,939
PRIOR FILING DATE: 2000-02-24
NUMBER OF SEQ ID NOS: 350
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 240
TYPE: PRT
ORGANISM: Homo sapiens
US-09-968-744A-2

Query Match      88.8%; Score 482; DB 12; Length 240;
Best Local Similarity 90.4%; Pred. No. 1,1e-36;
Matches 94; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 2 MTQSPSSLSASVGDVAVTTTCRASQSIIRYLNWYQHKRGPAPKLLIHTASSLSQGVSPSRFS 61
DB 136 MTQSPSSLSASVGDVAVTTTCRASQSIIRYLNWYQHKRGPAPKLLIHTASSLSQGVSPSRFS 195

QY 62 GSVSGTDFLTITSSLSQPEDFATYYCQOSYTTPTFGGQTKLQIK 105
DB 196 GSVSGTDFLTITSSLSQPEDFATYYCQOSYTTPTFGGQTKVEIK 239

RESULT 12
US-09-848-798-44
Sequence 44, Application US/09848798
Publication No. US20030040605A1
GENERAL INFORMATION:
APPLICANT: Siegel, Donald L
TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
FILE REFERENCE: 09596-4202
CURRENT APPLICATION NUMBER: US/09/848,798
CURRENT FILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 44
LENGTH: 107
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: anti-Rh(D) chain 113
US-09-848-798-44

Query Match      88.6%; Score 481; DB 11; Length 107;
Best Local Similarity 89.4%; Pred. No. 5,9e-37;
Matches 93; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 2 MTQSPSSLSASVGDVAVTTTCRASQSIIRYLNWYQHKRGPAPKLLIHTASSLSQGVSPSRFS 61
DB 3 MTQSPSSLSASVGDVAVTTTCRASQSIIRYLNWYQHKRGPAPKLLIHTASSLSQGVSPSRFS 62

QY 62 GSVSGTDFLTITSSLSQPEDFATYYCQOSYTTPTFGGQTKLQIK 105
DB 63 GSVSGTDFLTITSSLSQPEDFATYYCQOSYTTPTFGGQTKLQIK 106
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RESULT 13
US-09-848-798-32
Sequence 32, Application US/09848798
Publication No. US20030040605A1
GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
FILE REFERENCE: 09596-42U2
CURRENT FILING DATE: 2001-05-04
PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: PatentIn Ver. 2.0
LENGTH: 108
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: anti-Rh(D) chain 101
US-09-848-798-32

Query Match
Best Local Similarity 88.5%; Score 480.5; DB 11; Length 108;
Best Local Similarity 90.5%; Pred. No. 6,7e-37;
Matches 95; Conservative 4; Mismatches 5; Indels 1; Gaps 1;

QY 2 MTQSPSSLSASVGDRTVITTCRASQSIIRYLNWYQHKPKKLLHTTASLSGVSRRFS 61
DB 3 LTQSPSSLSASVGDRTVITTCRASQSIIRYLNWYQHKPKKLLHTTASLSGVSRRFS 62

QY 62 GSVSGTDFLTITSSLOPEDFATYYCOQSYTT-PYTFGQGTKLQIK 105
DB 63 GSGSGTDFLTITSSLOPEDFATYYCOQSYTPTTFGQGTKLQIK 107

RESULT 14
US-09-848-798-43
Sequence 43, Application US/09848798
Publication No. US20030040605A1
GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
FILE REFERENCE: 09596-42U2
CURRENT FILING DATE: 2001-05-04
PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: PatentIn Ver. 2.0
LENGTH: 108
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: anti-Rh(D) chain 112
US-09-848-798-43

Query Match
Best Local Similarity 88.5%; Score 480.5; DB 11; Length 108;
Best Local Similarity 90.5%; Pred. No. 6,7e-37;
Matches 95; Conservative 4; Mismatches 5; Indels 1; Gaps 1;

QY 2 MTQSPSSLSASVGDRTVITTCRASQSIIRYLNWYQHKPKKLLHTTASLSGVSRRFS 61
DB 3 LTQSPSSLSASVGDRTVITTCRASQSIIRYLNWYQHKPKKLLHTTASLSGVSRRFS 62

QY 62 GSVSGTDFLTITSSLOPEDFATYYCOQSYTT-PYTFGQGTKLQIK 105
DB 63 GSGSGTDFLTITSSLOPEDFATYYCOQSYTPTTFGQGTKLQIK 107

RESULT 15
US-09-848-798-37
Sequence 37, Application US/09848798
Publication No. US20030040605A1
GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
FILE REFERENCE: 09596-42U2
CURRENT FILING DATE: 2001-05-04
PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: PatentIn Ver. 2.0
LENGTH: 107
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: anti-Rh(D) chain 106
US-09-848-798-37

Query Match
Best Local Similarity 88.4%; Score 480; DB 11; Length 107;
Best Local Similarity 89.4%; Pred. No. 7,3e-37;
Matches 93; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 2 MTQSPSSLSASVGDRTVITTCRASQSIIRYLNWYQHKPKKLLHTTASLSGVSRRFS 61
DB 3 LTQSPSSLSASVGDRTVITTCRASQSIIRYLNWYQHKPKKLLHTTASLSGVSRRFS 62

QY 62 GSVSGTDFLTITSSLOPEDFATYYCOQSYTPTTFGQGTKLQIK 105
DB 63 GSGSGTDFLTITSSLOPEDFATYYCOQSYTPTTFGQGTKLQIK 106

Search completed: January 22, 2004, 12:00:42
Job time : 32.5 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 22, 2004, 11:50:06 ; Search time 12.7826 Seconds
(without alignments)
347.553 Million cell updates/sec

Title: US-09-147-443D-60
Perfect score: 543
Sequence: 1 VMTQSPSSLSASVGDRTIT.....CQGSYTPYFGQGLQIK 105

Scoring table: BLOSUM62
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Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
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| 1 | 491 | 90.4 | 107 | 1 US-08-276-852-104 | Sequence 104, App |
| 2 | 491 | 90.4 | 107 | 1 US-08-899-575-104 | Sequence 104, App |
| 3 | 491 | 90.4 | 107 | 1 US-08-899-575-104 | Sequence 104, App |
| 4 | 491 | 90.4 | 107 | 5 PCT-US95-08743-104 | Sequence 104, App |
| 5 | 487 | 89.7 | 107 | 3 US-09-240-274-36 | Sequence 36, Appl |
| 6 | 487 | 89.7 | 107 | 3 US-09-240-274-156 | Sequence 156, App |
| 7 | 483 | 89.0 | 107 | 1 US-08-276-852-105 | Sequence 105, App |
| 8 | 483 | 89.0 | 107 | 1 US-08-899-575-105 | Sequence 105, App |
| 9 | 483 | 89.0 | 107 | 5 PCT-US95-08743-105 | Sequence 105, App |
| 10 | 483 | 88.8 | 107 | 3 US-09-240-274-175 | Sequence 175, App |
| 11 | 482 | 88.8 | 107 | 3 US-09-240-274-176 | Sequence 176, App |
| 12 | 482 | 88.8 | 107 | 3 US-09-240-274-44 | Sequence 44, Appl |
| 13 | 480.5 | 88.5 | 108 | 3 US-09-240-274-32 | Sequence 32, Appl |
| 14 | 480.5 | 88.5 | 108 | 3 US-09-240-274-33 | Sequence 33, Appl |
| 15 | 480.5 | 88.4 | 107 | 3 US-09-240-274-37 | Sequence 37, Appl |
| 16 | 480 | 88.2 | 107 | 3 US-09-240-274-179 | Sequence 179, App |
| 17 | 479 | 87.8 | 104 | 1 US-08-276-852-106 | Sequence 106, App |
| 18 | 477 | 87.8 | 104 | 1 US-08-899-575-106 | Sequence 106, App |
| 19 | 477 | 87.8 | 104 | 1 US-08-899-575-106 | Sequence 106, App |
| 20 | 477 | 87.8 | 104 | 5 PCT-US95-08743-106 | Sequence 106, App |
| 21 | 476.5 | 87.8 | 108 | 3 US-09-240-274-167 | Sequence 167, App |
| 22 | 476.5 | 87.8 | 108 | 2 US-08-276-852-103 | Sequence 29, Appl |
| 23 | 476 | 87.7 | 107 | 1 US-08-899-575-103 | Sequence 103, App |
| 24 | 474 | 87.3 | 107 | 1 US-08-899-575-103 | Sequence 103, App |
| 25 | 474 | 87.3 | 107 | 1 US-08-899-575-103 | Sequence 103, App |
| 26 | 474 | 87.3 | 107 | 5 PCT-US95-08743-103 | Sequence 103, App |
| 27 | 474 | 87.3 | 107 | 5 PCT-US95-08743-103 | Sequence 103, App |

| | | | | | |
|----|-------|------|-----|---------------------|-------------------|
| 28 | 473 | 87.1 | 107 | 3 US-09-240-274-33 | Sequence 33, Appl |
| 29 | 472 | 86.9 | 107 | 3 US-09-240-274-38 | Sequence 38, Appl |
| 30 | 472 | 86.9 | 107 | 3 US-09-240-274-39 | Sequence 39, Appl |
| 31 | 471 | 86.7 | 107 | 3 US-09-240-274-158 | Sequence 158, App |
| 32 | 471 | 86.7 | 108 | 4 US-09-025-7698-14 | Sequence 14, Appl |
| 33 | 468 | 86.2 | 109 | 4 US-09-025-7698-28 | Sequence 28, Appl |
| 34 | 468 | 86.2 | 109 | 1 US-09-025-7698-43 | Sequence 43, Appl |
| 35 | 467 | 86.0 | 109 | 1 US-08-300-386A-43 | Sequence 69, Appl |
| 36 | 467 | 86.0 | 109 | 3 US-08-931-645-69 | Sequence 69, Appl |
| 37 | 467 | 86.0 | 109 | 5 PCT-US95-11235-69 | Sequence 69, Appl |
| 38 | 466.5 | 85.9 | 108 | 3 US-09-240-274-181 | Sequence 181, App |
| 39 | 466 | 85.8 | 107 | 3 US-09-240-274-35 | Sequence 35, Appl |
| 40 | 465 | 85.6 | 107 | 1 US-08-300-386A-66 | Sequence 66, Appl |
| 41 | 465 | 85.6 | 107 | 3 US-08-931-645-66 | Sequence 66, Appl |
| 42 | 465 | 85.6 | 107 | 3 US-09-240-274-173 | Sequence 173, App |
| 43 | 465 | 85.6 | 107 | 5 PCT-US95-11235-66 | Sequence 66, Appl |
| 44 | 464 | 85.5 | 109 | 3 US-09-157-370-3 | Sequence 31, Appl |
| 45 | 463.5 | 85.4 | 108 | 3 US-09-240-274-41 | Sequence 41, Appl |

ALIGNMENTS

RESULT 1
US-08-276-852-104
; Sequence 104, Application US/08276852
; Patent No. 5652138
; GENERAL INFORMATION:
; APPLICANT: Burton, Dennis R
; APPLICANT: Barbas, Carlos F
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; NUMBER OF SEQUENCES: 170
; CORRESPONDENCE ADDRESS:
; ADDRESSER: The Scripps Research Institute, Office of
; STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220,
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/276,852
; FILING DATE: 18-JUL-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/178,302
; FILING DATE: 30-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/954,148
; FILING DATE: 30-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: SCRL452P
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 104:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-276-852-104

Query Match 90.4%; Score 491; DB 1; Length 107;
Best Local Similarity 91.3%; Pred. No. 7.7e-37;
Matches 95; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 2 MTGSPSSLSASVGDVVTITCRASQSIIRYLNWYQHKPKAPKLLIHTASSLSQGVPSRFS 61
DB 2 LTGSPSSLSASVGDVVTITCRASQSIIRYLNWYQHKPKAPKLLIHTASSLSQGVPSRFS 61

QY 62 GSVGCTDFTLTISLQPEDFATYCCQSYTPTFFGGTKLQIK 105
DB 62 GSGGTDFTLTISLQPEDFATYCCQSYTPTFFGGTKLEIK 105

RESULT 2
US-08-899-575-104
; Sequence 104, Application US/08899575
; Patent No. 5770440
; GENERAL INFORMATION:
; APPLICANT: Burton, Dennis R
; APPLICANT: Barbas, Carlos F
; APPLICANT: Lerner, Richard A
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 170
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESS: Patent Counsel
; STREET: 10666 No. 5770440th Torrey Pines Road, Suite 220,
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/899,575
; FILING DATE: 24-JUL-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/276,852
; FILING DATE: 18-JUL-1994
; APPLICATION NUMBER: US 08/178,302
; FILING DATE: 30-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/954,148
; FILING DATE: 30-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: SC1452P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 104:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-899-575-104

Query Match 90.4%; Score 491; DB 1; Length 107;
Best Local Similarity 91.3%; Pred. No. 7.7e-37;
Matches 95; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 2 MTGSPSSLSASVGDVVTITCRASQSIIRYLNWYQHKPKAPKLLIHTASSLSQGVPSRFS 61
DB 2 LTGSPSSLSASVGDVVTITCRASQSIIRYLNWYQHKPKAPKLLIHTASSLSQGVPSRFS 61

QY 62 GSVGCTDFTLTISLQPEDFATYCCQSYTPTFFGGTKLQIK 105
DB 62 GSGGTDFTLTISLQPEDFATYCCQSYTPTFFGGTKLEIK 105

RESULT 3
US-08-899-575-104
; Sequence 104, Application US/08899575
; Patent No. 5804440
; GENERAL INFORMATION:
; APPLICANT: Burton, Dennis R
; APPLICANT: Barbas, Carlos F
; APPLICANT: Lerner, Richard A
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 170
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESS: Patent Counsel
; STREET: 10666 No. 5804440th Torrey Pines Road, Suite 220,
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/899,575
; FILING DATE: 24-JUL-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/276,852
; FILING DATE: 18-JUL-1994
; APPLICATION NUMBER: US 08/178,302
; FILING DATE: 30-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/954,148
; FILING DATE: 30-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: SC1452P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 104:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-899-575-104

Query Match 90.4%; Score 491; DB 1; Length 107;
Best Local Similarity 91.3%; Pred. No. 7.7e-37;
Matches 95; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 2 MTGSPSSLSASVGDVVTITCRASQSIIRYLNWYQHKPKAPKLLIHTASSLSQGVPSRFS 61
DB 2 LTGSPSSLSASVGDVVTITCRASQSIIRYLNWYQHKPKAPKLLIHTASSLSQGVPSRFS 61

QY 62 GSVGCTDFTLTISLQPEDFATYCCQSYTPTFFGGTKLQIK 105
DB 62 GSGGTDFTLTISLQPEDFATYCCQSYTPTFFGGTKLEIK 105

RESULT 4
PCT-US95-08743-104
; Sequence 104, Application PC/TUS9508743

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GENERAL INFORMATION:
APPLICANT: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
NUMBER OF SEQUENCES: 170
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/08743
FILING DATE: 11-JUL-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/276,852
FILING DATE: 18-JUL-1994
INFORMATION FOR SEQ ID NO: 104:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-08743-104

Query Match      90.4%; Score 491; DB 5; Length 107;
Best Local Similarity 91.3%; Pred. No. 7,7e-37;
Matches 95; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 2 MTQSPSSISASVGDRTTTCRASQSIIRYLNWYQHKRGKAPKLLITASSLQGVPSRFS 61
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Db 2 LTQSPSSISASVGDRTTTCRASQSIIRYLNWYQHKRGKAPKLLITASSLQGVPSRFS 61
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 62 GSVSGTDTFTLTISLQPEDPATYCCQSYTTPYTFGGTGLQIK 105
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 62 GSGSGTDTFTLTISLQPEDPATYCCQSYTTPYTFGGTGLQIK 105
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 5
US-09-240-274-36
; Sequence 36, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 36
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain 105
US-09-240-274-36

Query Match      89.7%; Score 487; DB 3; Length 107;
Best Local Similarity 90.4%; Pred. No. 1,7e-36;
Matches 94; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 2 MTQSPSSISASVGDRTTTCRASQSIIRYLNWYQHKRGKAPKLLITASSLQGVPSRFS 61
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 3 LTQSPSSISASVGDRTTTCRASQSIIRYLNWYQHKRGKAPKLLITASSLQGVPSRFS 62
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 62 GSVSGTDTFTLTISLQPEDPATYCCQSYTTPYTFGGTGLQIK 105
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 63 GSGSGTDTFTLTISLQPEDPATYCCQSYTTPYTFGGTGLQIK 106
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```

```
RESULT 6
US-09-240-274-156
; Sequence 156, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 156
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH13
US-09-240-274-156

Query Match      89.7%; Score 487; DB 3; Length 107;
Best Local Similarity 90.4%; Pred. No. 1,7e-36;
Matches 94; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 2 MTQSPSSISASVGDRTTTCRASQSIIRYLNWYQHKRGKAPKLLITASSLQGVPSRFS 61
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 3 LTQSPSSISASVGDRTTTCRASQSIIRYLNWYQHKRGKAPKLLITASSLQGVPSRFS 62
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 62 GSVSGTDTFTLTISLQPEDPATYCCQSYTTPYTFGGTGLQIK 105
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 63 GSGSGTDTFTLTISLQPEDPATYCCQSYTTPYTFGGTGLQIK 106
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RESULT 7
US-08-276-852-105
; Sequence 105, Application US/08276852
; Patent No. 5652138
; GENERAL INFORMATION:
; APPLICANT: Burton, Dennis R
; APPLICANT: Barbas, Carlos F
; APPLICANT: Lerner, Richard A
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 170
; CORRESPONDENCE ADDRESS:
; ADDRESS: The Scripps Research Institute, Office of
; STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220,
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/276,852
; FILING DATE: 18-JUL-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/178,302
; FILING DATE: 30-SEP-1993
; PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US 07/954,148
FILING DATE: 30-SEP-1992
ATTORNEY/AGENT INFORMATION:
  NAME: Fitting, Thomas
  REGISTRATION NUMBER: 34,163
  REFERENCE/DOCKET NUMBER: SCRL452P
  TELECOMMUNICATION INFORMATION:
    TELEPHONE: 619-554-2937
    TELEFAX: 619-554-6312
  INFORMATION FOR SEQ ID NO: 105:
    SEQUENCE CHARACTERISTICS:
      LENGTH: 107 amino acids
      TYPE: amino acid
      TOPOLOGY: linear
    MOLECULE TYPE: protein
  US-08-276-852-105

Query Match      89.0%; Score 483; DB 1; Length 107;
Best Local Similarity 90.4%; Pred. No. 3,9e-36;
Matches 94; Conservative 4; Mismatches 6; Indels 0; Gaps 0.

QY      2 MTGSSSLASVSGRVITTCRASQSIIRYLNWYQHHPKAPKLHITNASSLQSGVPSRFS 61
       :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      2 LTGSPSSLSASVSGRVITTCRASQSISSYLNWYQOKPKAPKLHITNASSLQSGVPSRFS 61
QY      62 GSVGCTDFTLTSSLSQPEDFATYYCOQSYTPPTTGGCTKXQIK 105
       :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      62 GSGGCTDFTLTSSLSQPEDFATYYCOQSYSTPPTTGGCTKLEIK 105

RESULT 8
US-08-899-575-105
; Sequence 105, Application US/08899575
; Patent No. 5770440
; GENERAL INFORMATION:
  APPLICANT: Burton, Dennis R
  APPLICANT: Barbas, Carlos P
  APPLICANT: Lerner, Richard A
  TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
  TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
  NUMBER OF SEQUENCES: 170
  CORRESPONDENCE ADDRESS:
    ADDRESSSEE: The Scripps Research Institute, Office of
    ADDRESSSEE: Patent Counsel
    STREET: 10666 No. 5770440th Torrey Pines Road, Suite 220,
    STREET: Mail Drop TPC8
    CITY: La Jolla
    STATE: CA
    COUNTRY: USA
    ZIP: 92037
  COMPUTER READABLE FORM:
    MEDIUM TYPE: floppy disk
    COMPUTER: IBM PC compatible
    OPERATING SYSTEM: PC-DOS/MS-DOS
    SOFTWARE: PatentIn Release #1.0, Version #1.25
  CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/08/899,575
    FILING DATE: 24-JUL-1997
  CLASSIFICATION: 435
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: US 08/276,852
    FILING DATE: 18-JUL-1994
    APPLICATION NUMBER: US 08/178,102
    FILING DATE: 30-SEP-1993
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: US 07/954,148
    FILING DATE: 30-SEP-1992
    ATTORNEY/AGENT INFORMATION:
      NAME: Fitting, Thomas
      REGISTRATION NUMBER: 34,163
      REFERENCE/DOCKET NUMBER: SCRL452P
      TELECOMMUNICATION INFORMATION:
        TELEPHONE: 619-554-2937

```

```

TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 105:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-899-575-105

Query Match      89.0%; Score 483; DB 1; Length 107;
Best Local Similarity 90.4%; Pred. No. 3,9e-36;
Matches 94; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY      2 MTQSPSLASVGDRTYITTCRASQSIIRYINWYQHKPKGAPKLLIHVASSLSQGVSPSRFS 61
      1:|||||
Db      2 LTQSPSLASVGDRTYITTCRASQSIISYINWYQHKPKGAPKLLIHVASSLSQGVSPSRFS 61
      1:|||||
      62 GSGSGTDFLTLLTISLQPEDPATYCYCQSQSYTPGFGGTLEIK 105
      1:|||||

RESULT 9
US-08-899-575-105
Sequence 105, Application US/08899575
Patent No. 5804440
GENERAL INFORMATION:
APPLICANT: Burton, Dennis R
APPLICANT: Barbas, Carlos F
APPLICANT: Lerner, Richard A
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
NUMBER OF SEQUENCES: 170
CORRESPONDENCE ADDRESS:
ADDRESSSEE: The Scripps Research Institute, Office of
ADDRESSSEE: Patent Counsel
STREET: 10666 No. 5804440th Torrey Pines Road, Suite 220,
STREET: Mail Drop TPC8
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/899,575
FILING DATE: 24-JUL-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/276,852
FILING DATE: 18-JUL-1994
APPLICATION NUMBER: US 08/178,302
FILING DATE: 30-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/954,148
FILING DATE: 30-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SCRI452P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 105:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-899-575-105

```

Query Match 89.0%; Score 483; DB 1; Length 107;
Best Local Similarity 90.4%; Pred. No. 3.9e-36;
Matches 94; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 2 MTQSPSSLSASVGDRTVITCRASQSIIRYLNWYQHKRGA PKLLIHTASSLSQGVPSRFS 61
:|||||
DB 2 LTQSPSSLSASVGDRTVITCRASQSIISYLNWYQKRGKAPKLLIYAASSLSQGVPSRFS 61
:|||||
QY 62 GSVSGTDFLTLLISLQPEDFATYCCQSYTTPYFGGKTLOIK 105
:|||||
DB 62 GSGSGTDFLTLLISLQPEDFATYCCQSYTTPYFGGKTLOIK 105
:|||||

RESULT 10
PCT-US95-08743-105
Sequence 105, Application PCT/TUS9508743

APPLICANT: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
NUMBER OF SEQUENCES: 170
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (ERO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/08743
FILING DATE: 11-JUL-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/276,852
FILING DATE: 18-JUL-1994
INFORMATION FOR SEQ ID NO: 105:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-08743-105

Query Match 89.0%; Score 483; DB 5; Length 107;
Best Local Similarity 90.4%; Pred. No. 3.9e-36;
Matches 94; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 2 MTQSPSSLSASVGDRTVITCRASQSIIRYLNWYQHKRGA PKLLIHTASSLSQGVPSRFS 61
:|||||
DB 2 LTQSPSSLSASVGDRTVITCRASQSIISYLNWYQKRGKAPKLLIYAASSLSQGVPSRFS 61
:|||||
QY 62 GSVSGTDFLTLLISLQPEDFATYCCQSYTTPYFGGKTLOIK 105
:|||||
DB 62 GSGSGTDFLTLLISLQPEDFATYCCQSYTTPYFGGKTLOIK 105
:|||||

RESULT 11
US-09-240-274-175
Sequence 175, Application US/09240274

APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
FILE REFERENCE: 09596-4202
CURRENT APPLICATION NUMBER: US/09/240,274
CURRENT FILING DATE: 1999-01-29
EARLIER APPLICATION NUMBER: 60/081,380
EARLIER FILING DATE: 1998-04-10
EARLIER APPLICATION NUMBER: 60/028,550
EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 175
LENGTH: 107

TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: anti-Rh(D) antibody clone SH49
US-09-240-274-175

Query Match 88.8%; Score 482; DB 3; Length 107;
Best Local Similarity 88.5%; Pred. No. 4.8e-36;
Matches 92; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 2 MTQSPSSLSASVGDRTVITCRASQSIIRYLNWYQHKRGA PKLLIHTASSLSQGVPSRFS 61
:|||||
DB 3 LTQSPSSLSASVGDRTVITCRASQSIISYLNWYQKRGKAPKLLIYAASSLSQGVPSRFS 62
:|||||
QY 62 GSVSGTDFLTLLISLQPEDFATYCCQSYTTPYFGGKTLOIK 105
:|||||
DB 63 GSGSGTDFLTLLISLQPEDFATYCCQSYTTPYFGGKTLOIK 106
:|||||

RESULT 12
US-09-240-274-176
Sequence 176, Application US/09240274

APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
FILE REFERENCE: 09596-4202
CURRENT APPLICATION NUMBER: US/09/240,274
CURRENT FILING DATE: 1999-01-29
EARLIER APPLICATION NUMBER: 60/081,380
EARLIER FILING DATE: 1998-04-10
EARLIER APPLICATION NUMBER: 60/028,550
EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 176
LENGTH: 107
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: anti-Rh(D) antibody clone SH50
US-09-240-274-176

Query Match 88.8%; Score 482; DB 3; Length 107;
Best Local Similarity 88.5%; Pred. No. 4.8e-36;
Matches 92; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 2 MTQSPSSLSASVGDRTVITCRASQSIIRYLNWYQHKRGA PKLLIHTASSLSQGVPSRFS 61
:|||||
DB 3 LTQSPSSLSASVGDRTVITCRASQSIISYLNWYQKRGKAPKLLIYAASSLSQGVPSRFS 62
:|||||
QY 62 GSVSGTDFLTLLISLQPEDFATYCCQSYTTPYFGGKTLOIK 105
:|||||
DB 63 GSGSGTDFLTLLISLQPEDFATYCCQSYTTPYFGGKTLOIK 106
:|||||

RESULT 13

US-09-240-274-44
Sequence 44, Application US/09240274
Patent No. 6255455
GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
FILE REFERENCE: 09596-4202
CURRENT APPLICATION NUMBER: US/09/240,274
CURRENT FILING DATE: 1999-01-29
EARLIER APPLICATION NUMBER: 60/081,380
EARLIER FILING DATE: 1998-04-10
EARLIER APPLICATION NUMBER: 60/028,550
EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224

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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 44
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain 113
US-09-240-274-44

Query Match      88.6%; Score 481; DB 3; Length 107;
Best Local Similarity 89.4%; Pred. No. 5.9e-36;
Matches 93; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 2 MTQSPSSLSASVGDRTVITTCRASQSIIRYLNWYOHKPKAKPLIHTASSLSQGVPSRFS 61
   |||||
DB 3 LTQSPSSLSASVGDRTVITTCRASQSIIRYLNWYOHKPKAKPLIHTASSLSQGVPSRFS 62
   |||||

QY 62 GSVSGTDFTLTITSSLOPEDFATYYCOOSYTTPTFGGQTKLQIK 105
   |||||
DB 63 GSGSGTDFTLTITSSLOPEDFATYYCOOSYTTPTFGGQTKLEIK 106
   |||||

RESULT 14
US-09-240-274-32
; Sequence 32, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/240,274
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 32
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain 101
US-09-240-274-32

Query Match      88.5%; Score 480.5; DB 3; Length 108;
Best Local Similarity 90.5%; Pred. No. 6.6e-36;
Matches 95; Conservative 4; Mismatches 5; Indels 1; Gaps 1;

QY 2 MTQSPSSLSASVGDRTVITTCRASQSIIRYLNWYOHKPKAKPLIHTASSLSQGVPSRFS 61
   |||||
DB 3 LTQSPSSLSASVGDRTVITTCRASQSIIRYLNWYOHKPKAKPLIHTASSLSQGVPSRFS 62
   |||||

QY 62 GSVSGTDFTLTITSSLOPEDFATYYCOOSYTTPTFGGQTKLQIK 105
   |||||
DB 63 GSGSGTDFTLTITSSLOPEDFATYYCOOSYTTPTFGGQTKLEIK 107
   |||||

RESULT 15
US-09-240-274-43
; Sequence 43, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/240,274
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
```

```
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 43
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain 112
US-09-240-274-43

Query Match      88.5%; Score 480.5; DB 3; Length 108;
Best Local Similarity 90.5%; Pred. No. 6.6e-36;
Matches 95; Conservative 4; Mismatches 5; Indels 1; Gaps 1;

QY 2 MTQSPSSLSASVGDRTVITTCRASQSIIRYLNWYOHKPKAKPLIHTASSLSQGVPSRFS 61
   |||||
DB 3 LTQSPSSLSASVGDRTVITTCRASQSIIRYLNWYOHKPKAKPLIHTASSLSQGVPSRFS 62
   |||||

QY 62 GSVSGTDFTLTITSSLOPEDFATYYCOOSYTTPTFGGQTKLQIK 105
   |||||
DB 63 GSGSGTDFTLTITSSLOPEDFATYYCOOSYTTPTFGGQTKLEIK 107
   |||||
```

Search completed: January 22, 2004, 11:54:21
Job time : 13.7826 secs

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OM protein - protein search, using sw model

Run on: January 22, 2004, 11:50:06 ; Search time 15.2174 Seconds
(without alignments)
347.553 Million cell updates/sec

Title: US-09-147-443D-58
Perfect score: 669
Sequence: 1 QVLLSSGGGVQPGGSLRV.....SRNYMDVKGKTTVYSS 125

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/prodata/2/1aa/5A_COMB.pep.*
2: /cgn2_6/prodata/2/1aa/5B_COMB.pep.*
3: /cgn2_6/prodata/2/1aa/6A_COMB.pep.*
4: /cgn2_6/prodata/2/1aa/6B_COMB.pep.*
5: /cgn2_6/prodata/2/1aa/PCTUS_COMB.pep.*
6: /cgn2_6/prodata/2/1aa/backfillset1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------------|
| 1 | 543.5 | 81.2 | 126 | 3 | US-09-240-274-152 |
| 2 | 543 | 81.2 | 125 | 3 | US-09-240-274-8 |
| 3 | 543 | 81.2 | 125 | 3 | US-09-240-274-20 |
| 4 | 543 | 81.2 | 125 | 3 | US-09-240-274-21 |
| 5 | 543 | 81.2 | 125 | 3 | US-09-240-274-22 |
| 6 | 542.5 | 81.1 | 126 | 3 | US-09-240-274-17 |
| 7 | 541.5 | 80.9 | 126 | 3 | US-09-240-274-14 |
| 8 | 541.5 | 80.9 | 126 | 3 | US-09-240-274-15 |
| 9 | 541.5 | 80.9 | 126 | 3 | US-09-240-274-147 |
| 10 | 541.5 | 80.9 | 126 | 3 | US-09-240-274-148 |
| 11 | 539.5 | 80.6 | 126 | 3 | US-09-240-274-16 |
| 12 | 535 | 80.0 | 126 | 3 | US-09-240-274-23 |
| 13 | 533 | 79.7 | 127 | 3 | US-09-240-274-139 |
| 14 | 530 | 79.2 | 127 | 3 | US-09-240-274-145 |
| 15 | 528 | 78.9 | 125 | 3 | US-09-240-274-9 |
| 16 | 527 | 78.8 | 125 | 3 | US-09-240-274-24 |
| 17 | 526.5 | 78.7 | 126 | 3 | US-09-240-274-26 |
| 18 | 524 | 78.3 | 127 | 3 | US-09-240-274-19 |
| 19 | 520.5 | 77.8 | 126 | 3 | US-09-240-274-153 |
| 20 | 519 | 77.6 | 127 | 3 | US-09-240-274-18 |
| 21 | 518.5 | 77.5 | 126 | 3 | US-09-240-274-25 |
| 22 | 517.5 | 77.4 | 126 | 3 | US-09-240-274-149 |
| 23 | 503.5 | 75.3 | 310 | 4 | US-09-079-029-11 |
| 24 | 503 | 75.2 | 125 | 3 | US-09-240-274-140 |
| 25 | 502.5 | 75.1 | 126 | 3 | US-09-240-274-140 |
| 26 | 502.5 | 75.1 | 126 | 3 | US-09-240-274-144 |
| 27 | 502.5 | 75.1 | 126 | 3 | US-09-240-274-150 |

| | | | | | | |
|----|-------|------|-----|---|-------------------|-------------------|
| 28 | 497.5 | 74.4 | 126 | 3 | US-09-240-274-146 | Sequence 146, App |
| 29 | 494 | 73.8 | 127 | 3 | US-09-240-274-11 | Sequence 11, Appl |
| 30 | 492.5 | 73.6 | 126 | 3 | US-09-240-274-13 | Sequence 13, Appl |
| 31 | 488 | 72.9 | 119 | 1 | US-08-331-398A-46 | Sequence 46, Appl |
| 32 | 488 | 72.9 | 119 | 2 | US-08-331-397B-46 | Sequence 46, Appl |
| 33 | 488 | 72.9 | 119 | 2 | US-08-759-804A-46 | Sequence 46, Appl |
| 34 | 488 | 72.9 | 119 | 3 | US-09-227-693-46 | Sequence 46, Appl |
| 35 | 487 | 72.8 | 121 | 3 | US-09-202-181-4 | Sequence 4, Appl |
| 36 | 481 | 71.9 | 142 | 1 | US-08-305-683A-2 | Sequence 2, Appl |
| 37 | 478 | 71.4 | 287 | 3 | US-08-862-124-17 | Sequence 17, Appl |
| 38 | 478 | 71.4 | 304 | 3 | US-08-862-124-14 | Sequence 14, Appl |
| 39 | 477 | 71.3 | 125 | 3 | US-09-240-274-151 | Sequence 151, App |
| 40 | 474 | 70.9 | 120 | 1 | US-07-942-245-35 | Sequence 35, Appl |
| 41 | 472.5 | 70.6 | 140 | 3 | US-08-983-607-32 | Sequence 32, Appl |
| 42 | 472 | 70.6 | 249 | 4 | US-10-039-785-53 | Sequence 53, Appl |
| 43 | 471.5 | 70.5 | 248 | 4 | US-09-315-926A-80 | Sequence 80, Appl |
| 44 | 470 | 70.3 | 123 | 4 | US-09-560-198A-2 | Sequence 2, Appl |
| 45 | 469.5 | 70.2 | 245 | 4 | US-08-918-148-76 | Sequence 76, Appl |

ALIGNMENTS

```
RESULT 1
US-09-240-274-152
; Sequence 152, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rn(D) - BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-4202
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 152
; LENGTH: 126
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH54
US-09-240-274-152

Query Match      81.2% Score 543.5; DB 3; Length 126;
Best Local Similarity 80.2% Pred. No. 8.4e-45;
Matches 101; Conservative 14; Mismatches 10; Indels 1; Gaps 1;

QY      1 QVLLSSGGGVQPGGSLRVACVAGFTFRNFGMHWROAPKGLBWAFFIPDASNKCY 60
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      1 EVQLLESGGCVQVQPSRLRLSCAAGFTFSRNGMHWROAPKGLBWAFFIPDGSNKYY 60
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      61 GSVVGRFTVPSDNRKNTLYLQMGRLRADPTAVVYCARBKAIRGSRNYMDVWGKGT 119
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      61 ADSVGRFTISDNRKNTLYLQMSLRADDAVYVYCARBKAIRGLTRSYGMDVWGQGT 120
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      120 TVTVSS 125
      : : : : :
DB      121 TVTVSS 126
      : : : : :

RESULT 2
US-09-240-274-8
; Sequence 8, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rn(D) - BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-4202
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 152
; LENGTH: 126
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH54
US-09-240-274-152
```

```

Db          121 VTWSS 125

RESULT 4
US-09-240-274-21
; Sequence 21, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/240,274
; EARLIER FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 125
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain D16
US-09-240-274-21

Query Match      81.2%; Score 543; DB 3; Length 125;
Best Local Similarity 80.0%; Pred. No. 9,2e-45;
Matches 100; Conservative 9; Mismatches 16; Indels 0; Gaps 0;

QY    1 QVKLBEGGGVVGPGSLRACVAGSGTFERNFGHWRORAPGKLEWVAFIWPDASNKGY 60
       :|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
DB     1 EVQLBESGGGVDPGRSLRLSCVVSGETFNNYGHWRAOPGKLEWVAVIWFDSNKKY 60
QY    61 GDSTVKGFTFSRDNSKNTLYLQNMGLRAPDPAVYYCARERAVRSIRNYMDVWGKGT 120
       |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
DB     61 ADSVKGFTFSRDNSKNTLYLQNMGLRAPDPAVYYCARERAVRSIRNYMDVWGKGT 120

QY    121 VTWSS 125
       |||||
DB     121 VTWSS 125

RESULT 5
US-09-240-274-22
; Sequence 22, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/240,274
; EARLIER FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
; LENGTH: 125
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain D17
US-09-240-274-22

Query Match      81.2%; Score 543; DB 3; Length 125;
Best Local Similarity 80.0%; Pred. No. 9,2e-45;
Matches 100; Conservative 9; Mismatches 16; Indels 0; Gaps 0;

```



```

? TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
? FILE REFERENCE: 09596-42U2
? CURRENT APPLICATION NUMBER: US/09/240,274
? EARLIER FILING DATE: 1999-01-29
? EARLIER FILING DATE: 1998-04-10
? EARLIER APPLICATION NUMBER: 60/081,380
? EARLIER FILING DATE: 1996-10-11
? NUMBER OF SEQ ID NOS: 224
? SOFTWARE: PatentIn Ver. 2.0
? SEQ ID NO 147
? LENGTH: 126
? TYPE: PRt
? ORGANISM: Homo sapiens
? FEATURE:
? OTHER INFORMATION: anti-Rh(D) antibody clone SH32
? IS-09-240-274-147
```

| | | | | |
|---------------------------|-------|--------------------|-----------|-------------|
| Query March | 80.9% | Score 541.5; | DB 3 | Length 126; |
| Best Local Similarity | 81.7% | Pred. No. 1,3e-44; | | |
| Matches 103; Conservative | 9; | Mismatches 13; | Indels 1; | Gaps 1. |

[illegible]

```

QY      61 GDSYKGRFTYSRDNSKNTLYLQNMGLRAEDPAVYVYAREKAVR-GTSRYNYMDVMWGSGT 119
        |||||
DQ      61 EDSYKGRFTYSRDNSKNTLYLQNMGLRAEDPAVYVYARELSKVALSRYYYIMDVMWGSGT 120
        |||||

```

| | | | |
|----|-----|--------|-----|
| QY | 120 | TVTVSS | 125 |
| | | | |
| Db | 121 | TVTSS | 126 |

```

RESULT 10
US-09-240-274-148
; Sequence 148, Application US/09240274
; Patent No. 625545
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELLS
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 148
; LENGTH: 126
; TYPE: PR1
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH37
; US-09-240-274-148

```

| | | | | |
|-----------------------|--------------|------------------|---------------|------------|
| Query Match | 80.9% | Score 541.5 | DB 3 | Length 126 |
| Best Local Similarity | 81.7% | Pred No. 1.3e-44 | | |
| Matches 103 | Conservative | 9 | Mismatches 13 | Indels 1 |
| | | | | Gaps 1 |

Dy QY 1 QVKLLESGGGVVQPGRSLRLVACASGFTPRNFGHMVRQAPBGKLEWAFIFPDASNKGX 60
:::|||||:::|||||:|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db 1 EVQLLES GGGVVQPGRSLRLSCASKFTDLYNGHMMVRQAPBGKLEWAFIFPDGSNKXY 60

```

Qy      61 GDSYKGRFTYSRDNSKNTLYIQMNGLRPAEDTAVYYCAREKAR-GISIKYNYNDWGKGT 119
      |||||
Db      61 EDYVAGRFTYSRDNSKNTLYIQMNSLRPAEDTAVYYCARELSKKVALSRYYYNDWGQGT 120

```

| | | | |
|----|-----|--------|-----|
| QY | 120 | TVTVSS | 125 |
| | | | |
| Db | 121 | TVTVSS | 126 |

RESULT 11
US-09-240-274-16
Sequence 16 Application US/09240274

APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF

```

1 CURRENT APPLICATION NUMBER: US/09/240,274
2
3 CURRENT FILING DATE: 1999-01-29
4
5 EARLIER APPLICATION NUMBER: 60/061,380
6
7 EARLIER FILING DATE: 1998-04-10
8
9 EARLIER APPLICATION NUMBER: 60/028,550
10
11 EARLIER FILING DATE: 1996-10-11
12
13 NUMBER OF SEQ ID NOS: 224
14
15 SOFTWARE: PatentIn Ver. 2.0
16
17 SEQ ID NO: 16

```

OTHER INFORMATION: anti-Rh(D) chain DIS
US-09-240-274-16

| | | | | |
|---------------------------|-------|-----------------|-----------|------------|
| Query Match | 80.6% | Score 539.5 | DB 3 | Length 126 |
| Best Local Similarity | 81.0% | Pred. No. 26-44 | | |
| Matches 102; Conservative | 10; | Mismatches 13; | Indels 1; | Gaps 1. |

[illegible]

```
Dy      61 GDSYKGRFVTSRDNSKNITLYLQNMGLRAEDTAVVYCAREKAKVR-GISRYNYMDVMGKGST 119
        |||||
Db      61 ADSYKGRFIVSRDNSKNITLYLQNMSLRAEDTAVVYCAREYSKKLAISRYYYYMDVMGCGST 120
```

| | | | |
|----|-----|--------|-----|
| QY | 120 | TVTVSS | 125 |
| | | | |
| Db | 121 | TVTSS | 126 |

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RESULT 12
US-09-240-274-23
Sequence 23. Application US/09240274
Patent No. 6255455
GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELLS
TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
FILE REFERENCE: 09596-4202
CURRENT APPLICATION NUMBER: US/09/240,274
CURRENT FILING DATE: 1999-01-29
EARLIER APPLICATION NUMBER: 60/081,380
EARLIER FILING DATE: 1998-04-10
EARLIER APPLICATION NUMBER: 60/028,550
EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 23
LENGTH: 125
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
US-09-240-274-23

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Query Match 80.0%; Score 535; DB 3; Length 125

